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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
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Q30159
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T18324
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P85827
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Q14851
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T67164
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BRCA1 gene 5' tran
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Human interleukin-
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Clone pTB1284 enco
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Human RAD54 nuclei
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HC-contig derived
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Cdn-2 DNA. N
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ed BRCA1 geno
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                                                                                                                                                                                                                                                                         gene signatu
                                                                                                                                                                                                                                                                                                                                                                     deoxycytidyl
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ALIGNMENTS

Human HCMV inducible gene, SEQ ID NO 21.

HCMV inducible gene; cig; human; human cytomegalovirus; interferon; anti-viral therapy; anti-HCMV therapy; detection; diagnosis; drug screening; ds.

X33947; 30-JUN-1999

(first entry)

X33947 standard; DNA; 3200

ВP

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RESULT 2
Q95493/c
Q95493 standard; DNA; 6511
AC Q95493;
DT 21-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Homo sapiens.
WO9913075-A2.
18-MAR-1999; U18638.
08-SEP-1997; US-059725.
08-SEP-1997; US-058180.
(UYPR-) UNIV PRINCETON.
Cong J, Schenk T, Zhu H;
WPI; 99-243729/20.
                                                                              Human Cdn-2 DNA. Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes Claim 2; Page 143-147; 184pp; English.
This sequence represents a human gene of the invention, that is induced to express by both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The invention also relates to genes that are repressed in the presence of HCMV infection, designated HCMV-repressible genes (crg or crgs). The products can be used to obtain agents which can be used for anti-viral therapy, particularly anti-HCMV therapy. They can also be used for the development of drugs that would allow for higher
                                                                                                                                                                                                                                                                                                                                                                    dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products be used for detection, diagnosis and drug screening. Sequence 3200 BP; 972 A; 629 C; 742 G; 857 T;
                                                                     shock; lymphoma; eczema; ss.
W09515084-A
                                                       Homo sapiens
                                                                                                                                                                                                                                      380 CAGGAGTTCCAGACCAGCCTGGGCAA 405
                                                                                                                                                                                                                                                                 289 CAGGAGTTCCAGACCAGCCTGGGCAA 314
                                                                                                                                                                                                                                                                                                Conservative
                        Location/Qualifiers 3312. 3947
                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
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RESULT
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30-NOV-1994; U13930.
30-NOV-1993; US-150067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY I
                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. Sequence 84 BP; 33 A; 17 C; 15 G; 19 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig.5A-H; 66pp; English.

Cdn-2 cDNA was isolated from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1393 CAGGAGTTCCAGACCAGCCTGGGC 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-blased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                               Claim 1; Page 1942; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                   reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene signature HUMGS08078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T25848 standard; cDNA to mRNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library - cor diagnosis of abnormal cell function, by preparing cDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 CAGGAGTTCCAGACCAGCCTGGGC 312
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Pred. No.
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Query Match Best Local Similarity

6.6%;

Score 23; Pred. No.

DB 1; 0.0056;

Length 84;

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RESULT
T15455
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V39298/c
       PPR PD PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a specifically claimed partial nucleic CC acid sequence encoding human RAD54 (hRAD54). A method for analysing a CC sample for mutation of DNA encoding hRAD54 has been developed using a CC DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present CC in tumours that display allelic imbalance at 1p32, the chromosomal band cidentified as one of four minimal regions of chromosome 1 deletion in CC breast carcinomas. hRAD54 is useful for production of proteins, inter CC alia, that have been identified as novel hRAD54 by homology between the CC amino acid sequence given in W62186 and known amino acid sequences such CC as yeast RAD54 proteins are used in the treatment of cancer. CC including Xeroderma Pigmentosum and Bloom syndrome, Werner's syndromes CC and X-linked mental retardation with alpha-thalassaemia syndrome and breast cancer. hRAD54 polynucleotides are also useful for detecting complementary nucleotides for use as a diagnostic agent, especially cuseful for diagnosis of disease or susceptibility to diseases, hRAD54 polynucleotides are also useful for detecting complementary proteins, agonists and antagonists which are proteins are useful in gene therapy.

So Sequence 840 BP; 190 A; 200 C; 221 G; 229 T;
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Homo sapiens.
W09602552-A1.
01-FEB-1996.
19-JUL-1995; U09145.
19-JUL-1994; US-276919.
                                                                                       Non-small cell lung cancer; NSCLC; tumour marker; carbonic anhydrase; diagnosis; therapy; promoter; fluorescent in situ hybridisation; ds.
                                                                                                                        23-APR-1996 (first entry)
Lung cancer specific antigen HCAVIII promoter region genomic tumour marker; HCAVIII;
                                                                                                                                                                               T15455 standard; DNA; 1363
T15455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP.
(UVJE-) UNIV JEFFERSON THOMAS.
CIOCGE CM, Fishel RA, Rasio D, Robbins DJ:
WPI: 98-274189/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonists, etc.
Claim 1; Page 28; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAY-1998.
10-NOV-1997; 308998.
13-NOV-1996; US-030676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hRAD54 DNA and polypeptide - and agonists, antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V39298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP-844305-A2.
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nucleic acid s
                                                                                                      diagnosis; therapy; promoter; DNA probe;
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Pred. No.
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27-APR-1990; JP-113146.
31-JUL-1990; JP-204438.
14-SEP-1990; JP-245256.
28-DEC-1990; JP-415801.
                                                                                                                                                                                                                                                                                                            New mutein(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 8; 88pp; English.

A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to maino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUCl18/119 to give pTB1228 (see Q14848). The complete FGF coding sequence was obtained by ligating the insert from pTB1228 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from GD11533 onwards.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer Claim 53; Page 62-63; Page; English.

A genomic clone (T15455) was isolated that constitutes the putative promoter of the HCAVIII gene (see T15448), and probably contains transcription regulatory elements directly implicated in expression of HCAVIII, a cell surface antigen which is highly specific for non-small cell lung carcinoma and which has features in common with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human carbonic anhydrases. The clone was obtd. by PCR amplification using a primer pair (T15456-57) based on the putative exon 6 of the HCAVIII gene. A DNA probe comprising the genomic clone plus flanking sequences was used for fluorescent in situ hybridisation. Sequence 1363 BP; 352 A; 382 C; 369 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEMICAL IND KI
Igarashi K, Senoo M, Watanabe
WPI; 91-353723/48.
P-PSDB; R15269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone pTB1283 encoding complete FGF receptor. Human; fibroblast growth factor; cancer; ss.
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                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                              2310 BP;
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                                                                                                                                                           Conservative
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Pred. No.
                                                                                                                                                                                    Score 22;
Pred. No.
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0.02;
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0.021;
                                                                                                                                                                                                                                                                                           636 G;
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T67164/c
TD T67164 standard; cDNA; 10380
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Best Local 9
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14-NOV-1991,
25-APR-1991, J00557.
27-APR-1990, JP-113146.
31-JUL-1990, JP-204438.
14-SEP-1990, JP-245256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New muterin(3) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 7; 88pp; English.

A cDNA library prepared from human cancer cell line Kato III mRNA A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1229 (see 014849). The complete FGF coding sequence was obtained by ligating the insert from pTB1229 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from pTB1281.
                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-1997 (first entry)
Human alpha-N-acetylglucosaminidase gene.
Alpha-N-acetylglucosaminidase; mucopolysa
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(TAKE) TAKEDA CHEMICAL IND KK.
IGARAShi K. Senoo M. Watanabe T;
WPI; 91-353723/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
Homo sapiens
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1373. วาว
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2263. .3055
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3203. .3386
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2115. .
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990. .1372
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Pred. No.
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0.021;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            hydrolyse the terminal alpha-N-acetylglucosamine residues at the non-reducing terminus of fragments of heparan sulphate and heparin. It was isolated by hybridisation of a human chromosome 17 library. A cDNA clone (T67163) coding for the enzyme has also been isolated. The isolated gene or cDNA, and primers/probes based on them or their complementary strands, can be used to investigate, diagnose and treat alpha-N-acetylglucosaminidase deficiency, for example in patients suffering from mucopolysacchariosis type IIIB.
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 W09315196-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W18017.

Nucleic acid encoding mammalian alpha-N-acetylglucosaminidase - used for the diagnosis and treatment of mucopolysaccharidosis type IIIB, also used in gene therapy Claim 8; Page 54-61; 79pp; English.

A genomic DNA molecule (T67164) includes 6 exons that code for human alpha-N-acetylglucosaminidase (W18017), an enzyme that can human alpha-N-acetylglucosaminidase (W18017).
                                                                                                                exon
                                                                                                                                                                                            Q46852;
26-JAN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Administration is by oral, i.v., i.p., enzyme replacement therapy, gene therapy or other routes.

Sequence 10380 BP; 2210 A; 2953 C; 2851 G; 2366 T;
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23-NOV-1995; AU-006748.
(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Anson DS, Blanch L, Hopwood JJ, Sco
WPI; 97-298114/27.
                                                                                                                                                                      Casein; supplement; milk; pharmaceutical;
                                                                                                                                                                                Clone of recombinant human kappa casein gene fragment.
                                             intron
                                                                                          intron
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                  Q46852 standard; DNA; 13104
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                                                                                                                                                                                                                                                                                                                                  Similarity
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5667. . sc.
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3473. sc
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8966. .10380
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8835.
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12278.
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Pred. No.
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0.022;
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RESULT
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ID T7
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Best Local
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                                                                                                                                                                                                                                       The present sequence encodes the human deoxycytidylate (dCMP) deaminase intron 2, which comprises 20303 base pairs from nucleotides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The recombinant human kappa casein is produced in high yields by means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can also be used as a pharmaceutical.

Sequence 13104 BP; 4256 A; 2497 C; 2397 G; 3953 T:
T71696 standard; DNA; 26764 T71696;
                                                                                                                                                                                                                                                                                                                                  DNA encoding human deoxycytidylate deaminase - for production recombinant deaminase claim 2; Column 83-100; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                            (HEAL-) HEALTH RES INC Maley F, Maley GR, WG WPI; 97-244391/22.
                                                                                                                                                                                                    to mutagenesis.
Sequence 20303 BP;
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10-JAN-1995; 370975.
10-JAN-1995; US-370975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human deoxycytidylate deaminase Recombinant deaminase; dCMP; ds.
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WPI; 93-258675/32.
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                                                                                                                                                                                                                             removed or mutated) to alter DNA replication in cells,
                                                                                                       289 CAGGAGTTCCAGACCAGCCTGG
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                                                                             CAGGAGTTCCAGACCAGCCTGG 15305
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100.0%;
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20-AUG-1997 (first entry)

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Best Local
                                                                                                          Matches
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The present sequence encodes the human deoxycytidylate (dCMP) deaminase gene, which contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dt Also, the dCMP gene can be altered (removed or mutated) to alter Dr replication in cells, which may lead to mutagenesis.

Sequence 26764 BP; 7079 A; 5521 C; 6539 G; 7625 T;
                                                                                                                                                                                                                                       DNA encoding human deoxycytidylate deaminase - recombinant deaminase
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10-JAN-1995;
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Human c-fms oncogene
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       17-JUN-1998
                 V20441;
                        V20441 standard;
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25392. .:
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                                                                                                        Score 22; DB; Pred. No. 0.0
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RESULT
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human chromosome 10, 10q25.2 region. Including an unusual chromosomal marker referred to as mardel(10). The an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional neocentromere at a location regarded as non-centromeric. This neocentromere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype replicable, segregating nucleic acid that confers a specific phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-klt, c-met, c-trk, c-src, c-abl, bor-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fox, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLI/MTG8, E2A/prl and ALL-L/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.

Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anticancer composition comprising two anti-sense oligo:nucleotide(s) - targetting cytoplasmic and nuclear oncogene(s) Claim 1; Column 59-90; 92pp; English.
                                                                                                                                                                                                                                                                                                          New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NC-contig derived from mardel(10) on chromosome 10q25.2. Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
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                                                                                                                                                                                                                                 The present sequence represents the NC-contig derived human chromosome 10, 10q25.2 region. The sequence cont
                                                                                                                                                                                                                                                                            Claim 9; Fig 16A;
                                                                                                                                                                                                                                                                                                                                                                                Cancilla MR, Choo K, Du WPI; 99-009773/01.
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26-AUG-1997; AU-008791.
13-MAY-1997; AU-006784.
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15-SEP-1994;
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; antisense oligonucleotide; c-fms; ds.
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Db 27572 CAGGAGTTCCAGACCAGCCTGG 27593
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                               neccentrowere at a location regarded as non-centroweric. This neccentrowere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neccentrowere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g., therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27312 CAGGAGTTCCAGACCAGCCTGG 27333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80240 BP; 23102 A; 16537 C; 16747 G; 23846 T;
                                                                                                                                                                                                                                                                        production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to into the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80595 BP; 23183 A; 16613 C; 16824 G; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the HC-contig derived from normal human chromosome 10, 10q25.2 region. This region can be naturally mutated to produce an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1998; AU0352.
26-AUG-1997; AU-008791.
13-MAY-1997; AU-006784.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Cancilla MR, Choo K, Du Sart D;
WPI; 99-009773/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 6; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9851790-A1.
19-NOV-1998.
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                                                             289 CAGGAGTTCCAGACCAGCCTGG
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nes 22; Conserv
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived
                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from normal human chromosome 10q25.2 region
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T25057
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DE Human
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PF 11-NOV
PR 12-NOV
PR (ANTS/
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Search completed: October Job time: 7379 sec
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognishing different cell types.

Sequence 158 BP; 46 A; 35 C; 44 G; 30 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1759; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the contractions of the contractions of the contractions human tissues; synthesis of cDNA was initiated from the contractions of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T25057;
11-NOV-1996 (first entry)
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W09514772-A1.
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                                                                                                                                                                                                                                                                                                                                258 GGGAGGCCGAGGCAGGAAGAT 278
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Pred. No.
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0.065;
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Result No. Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Title: Perfect score: Run OM nucleic - nucleic search, using sw model Database : Post-processing: Listing first 45 summaries Total number of hits satisfying chosen parameters: Searched: Scoring table: Sequence: o o O 00000 C 0000 9 size : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score Query Match N_Geneseq_36:* 0 US-09-065-672-4_COPY_1_276
276
1 CTAAGGCGTGCAAACAGAGC.... OLIGO_NUC Gapop 60.0 , Gapext 60.0 October 3, 2000, 14:37:34; 311585 seqs, 125096042 residues GenCore version 4.5 Copyright (c) 1993 - 2000 Comp CTAAGGCGTGCAAACAGAGC......CGGGAGGCCGAGGCAGGAAG 11288 11358 14556 14557 15099 20199 22481 10000 110000 235033 237326 237326 237326 134 155 Length 332 338 406 541 632 688 688 2351 3523 3523 7146 DВ T72060 T7304060 X304060 V11854 V27017 V389313 Q90512 T11549 Q90512 T11658 X13304 X1 Q12226 V90303 Q59619 Q60129 V90043 V88129 T25057 V87076 X22242 N90541 IJ SUMMARIES ᄓ Compugen Search time 114.21 Seconds (without alignments) 604.614 Million cell updates/sec Ltd 623170 Hereditary haemoch
Hereditary haemoch
Human c-fos protei
Human gene signatu
Staphylococcus aur Human Duffy genomi Homo sapiens DNA f Nucleic acid seque CEA clone HindIII-Streptococcus pneu PEDF full length s Human SC3 DNA. Pro Sequence flanking Sequence flanking DNA encoding a hum Hereditary haemoch Continuation (2 of Carcinoembryonic a Enterococcus faeca Tumour rejection a CEA genomic clone. EST clone CW1510. EST clone FY354. N Human brain Expres N-alpha-acetyltran EST clone DK113. N DNA encoding Human gene signatu EST clone BJ66. Ne Description Human brain Human secreted 276 Expres ed pro

RESULT 2
V87076/c
ID V87076 standard; cDNA; 540 BI
AC V87076;
DT 27-APR-1999 (first entry)
DE EST clone BJ66.

ВP

B

Matches Query Match Best Local

1 Similarity 19; Conserv

Conservative

6.9%; >--100.0%; Pr

%; Score 19; DB %; Pred. No. 0.6 0; Mismatches

DB 1; 0.6;

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Gaps

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T25057 standard; cDNA to T25057; standard; cDNA to T25057; l1-NOV-1996 (first entr. l1-NOV-1996 (first entr. l1-NOV-1996 (first entr. l1-NOV-1996 (first entr. l1-NOV-1996; abnormal ce Hommo sapiens; w0951472-A1. 01-JUN-1995; l1-NOV-1994; J01916. 11-NOV-1994; J01916. 11-NOV-1995, J01916. 11-NOV-1995, J01916. 11-NOV-1995, J01916. 11-NOV-1995, J01916. 11-NOV-1995, J0	11666666666666666666666666666666666666
ndard; cDNA to first ent signature Hitture; messeng ning; mapping; abnormal of signature Hitture; messeng ning; mapping; abnormal of signature Hitture; messeng ning; abnormal of signature signature signature abuno elative obtaine elative ob	<u> </u>
andard; cDNA to mRNA; 96 (first entry) e signature HUMGSO718 ature; messenger RNA; coning; mapping; non-b ng; abnormal cell fun ensA1. 95; J01916. 94; J01916. 93; JP-355504. ATSUBARA K. KUBO K. K. Okubo K; K. Okubo K; K. Okubo K; ng gene signatures in celative abundance of relative abundance is uniqu '-oriented cDNAs hybr ucted sequence is uniqu '-oriented cDNAs hybr ucted so as to reflec mRNAs in the particu rance frequency of a d (esp. using primers) as a means of diagn of different cell typ 158 BP; 46 A;	268 1 271 1 2 2 3 3 4 1 1 3 3 4 2 1 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
NA; 158 BP. 71888. 71888. 71888. 71888. 71888. 71888. 71888. 71888. 718888. 718888 7188	Q61087 T22202 Q60189 Q60189 V86324 V86377 Q61371 Q61371 T26195 T26195 T26195 T26581 Q60394 Q61360 ALIGNMENTS
tive abundance; frequency; ry; diagnosis; detection; d human cDNA library - e.g. by preparing cDNA that RNA in specific human from the 7837 "GS" sequences to hybridise to part of d. The GS (Gene Signature) cDNA libraries prepared cDNA was initiated from the lie primer. Since the 3'- licular mRNA species, almost specific mRNAs. Each library y the relative abundance of from which it was derived. a cDNA library can be derived from the GS mal cell function or for 4 G; 30 T;	Human brain Expres Human gene signatu Human brain Expres Expres Human gene signatu EST clone HOLOT. N Human brain Expres EST clone EN10. Ne Human brain Expres Human gene signatu Human gene signatu Human brain Expres Human brain Expres

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В
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CC This sequence represents an expressed sequence tag (EST), and is a CC polynucleotide of the invention. The polynucleotides of the invention are CC all secreted EST sequences isolated from a variety of human tissue Bources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for CC treating, preventing or ameliorating medical conditions in humans and CC animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, family activity, themostatic cactivity, cadherin/tumour invasion suppressor activity, haemostatic activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The property of the cactivity anti-inflammatory can be suppressed activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
 22-JUL-1997;
22-JUL-1997;
22-JUL-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
                                                                                                                                                                                                                   15-JUL-1998;
18-AUG-1997;
16-JUL-1997;
                                                                                                                                                                                                                                                                                                            duman secreted protein gene 32 clone HJABC16.
Human; secreted protein; gene therapy; protein therapy; cancer; valuman; secreted protein; gene therapy; protein therapy; cancer; valuman; chromosome mapping; forensic; haematological disease; all inflammation; cell proliferation; viral infection; wound healing; modulation; appetite; behaviour; food additive; preservative; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
Sequence
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Agostino MJ, Jacobs K, Lav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1998.
10-APR-1998; U06954
10-APR-1997; US-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemotaxis; chemokinesis; haemostasis; gene therapy; throrreceptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                        X22242 standard; DNA; 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Racie LA, Spaulding V, Treacy M; WPI; 99-070076/06.
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                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity. The EST sequences are also stated to be useful for
                                                                                                                         16-JUL-1997;
16-JUL-1997;
                                                                                                                                                         16-JUL-1997;
16-JUL-1997;
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16-JUL-1997;
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              US-052872

US-052873

US-052875

US-053440

US-053441

US-053441

US-05342

US-053683

US-05724

US-05725
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US-052661.
US-052870.
US-052871.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lavallie ER, McCoy JM, Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein; haematopoiesis regulator; inhibin; tumour invasion suppressor; EST; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
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Pred. No. 0.62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour invasion suppressor; EST;
asis; gene therapy; thrombolysis;
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                                                                                                                                                                                                                                                                                                                                              allergy;
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RESULT
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Best Local (
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The invention relates to nucleic acid sequences (X22211 to X22282)

The invention relates to nucleic acid sequences (X22211 to X22282)

encoding human secreted proteins (Y01383 to Y01454). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 209138, 209139 or 209141. Host cells containing vectors comprising the nucleic acid sequences are used for the recombinant expression of the secreted proteins. The polynucleotide and amino acid sequences are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polynucleotides. The nucleic acid sequences, or its fragments, are useful for chromosome identification and sequences, or its fragments, are useful for chromosome identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences, e.g. autoimmune or haematological diseases, allergy, inflammation, cancer or other forms of cell proliferation, viral or o infections. The sequences may also be useful in wound healing, to modulate differentiation of embryonic stem cells, to modulate weight, appetite, behaviour etc. and as food additive or preservative. The present sequence represents a gene encoding a human secreted protein (see descriptor line for gene number and clone identification). Sequence 702 BP; 187 A; 154 C; 174 G; 183 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mapping; as antisense and triplex-forming therapeutics; in gene therapy; for (forensic) identification of individuals; as molecular weight markers; to identify related sequences or specific mRNA; in preparation of oligomers and to raise anti-DNA antibodies. Antibodies are useful as immunoassay reagents (including for in vivo imaging) and therapeutically to inhibit or activate particular polypeptides. A very wide range of disorders may be treated with the polynucleotide and polypeptide
                                  misc_feature
                                                                                                       misc_feature
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18-AUG-1997; US-055985.
18-AUG-1997; US-055989.
18-AUG-1997; US-056359.
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                                                                                                                                                                                                                                                               N-alpha-acetyl transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
Duan R, Feng P, Ferrie AM, Florence KA,
                                                                                                                                                                                                                                             protein N-acetylation
                                                                                                                                                                                                                                                                               DNA encoding N-alpha-acetyl
                                                                                                                                                                                                                                                                                                N90541;
28-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                    N90541 standard; recombinant DNA; 2703
                                                                                                                                                                                                                                                                                                                                                                                                                         441 TTCGGGAGGCCGAGGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G;
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542. .566
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971. .
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479. .515
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338. .392
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1007.
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Pred. No.
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diseases and ident
                                                                                                                                                                                                                                                               resistance;
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0.62;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pure N-alpha-acetyl transferase and DNA encoding it - cat acetylation of proteins and peptides, eg to stabilise pharmac or induce herbicide resistance in plants.

Claim 8; Page 50; fig 12b-e; 72pp; English.

DNA encodes N-alpha-actyl transferase, used for catalysing N-of peptides/proteins, eg to stabilise pharmaceuticals or to i herbicide resistance in plants. Features a - n are fragments from exonuclease III deletion. See also P91070.

Sequence 2703 BP; 943 A; 489 C; 530 G; 741 T;
Mutant N-alpha-acetyl-transferase - produced from Saccharomyces cerevisiae for use in amino acid sequence determn. Disclosure; Fig 1; 77pp; English. The AAAl gene is located on chromosome IV and is positioned adjacent to the 5' flanking sequence of the SIR2 gene. Cells contg. a mutated AAAl gene lack N-alpha-acetyltransferase activity and are used to express, in vitro a recombinant protein peptide lacking an acetyl gp. at the alpha-amino gp. or to produ heterologous proteins. The proteins produced have altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1989;
07-FEB-1988; US-153361.
08-FEB-1988; US-153361.
14-DEC-1988; US-284344.
(GEHO) The General Hospital Corporation.
5mith JA, Lee FVS.
WPI: 89-24908/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
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                                                                                                                                                                                                                                                      25-OCT-1989; US-426381.
(GEHO-) GEN HOSPITAL CORP.
Smith JA, Lee FJS;
WPI; 91-164219/22.
                                                                                                                                                                                                                                                                                                                                                      16-MAY-1991.
15-OCT-1990; U05883
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e pharmaceuticals
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                 them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhbin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           substrate specificity and thermal stability. sequence of such proteins and peptides can be Sequence 2724 BP; 953 A; 491 C; 5:
                                                                                                                 19/c
Q59619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries. Claim 1; Page 497; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human expressed sequence tag
The polynucleotide, which is a secreted EST, and the encoded pa
are predicted to have useful biological activities which would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agostino MJ, Jacobs K, Lavallie Racie LA, Spaulding V, Treacy M; WPI; 99-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
             Homo sapiens. W09316178-A.
                                                       Human brain Expressed Sequence Tag EST01488.
Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                        activity. The polynucleotide may also be useful for gene therapy Sequence 332 BP; 71 A; 83 C; 84 G; 94 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-alpha-acetylation characteristics, e.g. increased or decreased
                                          transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
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Homo sapiens.
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                                                                                    16-MAR-1994
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17; Conser
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100.0%; Pr
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                                                                                                                  338
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                                          locations; chromosomes;
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Pred. No.
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3 G; 74
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                                                                                                                                                                                                                                                                            Length 332;
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O60129/c
ID Q601
AC Q601
AC Q601
DT 16-M
DE Huma
KW Gene
KW Gene
KW Gene
KW Gene
CU 19-A
PH 12-F
PR 12
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Example 4; Page 204; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed gene on chromosomes, for individual or forensic identification, for mappin locations of disease-associated genes, for identification of tissue type, and for prepn. of antisenses sequences, probes and constructs. EST01488 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440.

Sequence 338 BP; 77 A; 106 C; 67 G; 87 T;
                                                                                                                                                                                                                                                                                                                                                                                The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue
                                                                                                                                                                                                                                                                  type, and for prepn. of antisense sequences, probes and constructs. EST02116 has a "poor" coding probability as evaluated using the coding region prediction program CRM. See also 059041-061440. Sequence 406 BP; 74 A; 97 C; 110 G; 124 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        markers for human genes transcribed of most human genes example 4; Page 286; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain Expressed Sequence Tag EST02116.
Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 93-272882/34.
Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate
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12-FEB-1993; U01294.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH.
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12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Adams MD, Moreno RF, Venter CJ;
                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1994 (first entry)
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les 17; Conserv
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                                                        ATTTCGGGAGGCCGAGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s MD, Moreno RF, Venter 93-272882/34.
ATTTCGGGAGGCCGAGG 21
                                                                                                                                                  Similarity
                                                                                                                   Conservative
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enter CJ;
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                                                                                                                                               Score 17;
Pred. No.
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Pred. No.
                                                                                                                   Mismatches
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7;
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V88129/C
ID V881
AC V881
DT 12-F
DE EST
KW Chem
KW Chem
KW Chem
OS Homo
PN W098
PD 10-A
PR 10-A
PR 10-A
PR 10-A
PR 10-B
PR 10-
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Best Local S
Matches 17
                     New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries Claim 1; Page 292; 641pp; English.

The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to the invention of the invention of the invention are all secreted EST sequences and proteins encoded by them are predicted to the invention of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.

Claim 1; Page 413; 618pp; English.

The present sequence represents a human expressed sequence tag (EST) The polynucleotide, which is a secreted EST, and the encoded proteir are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, insurance activity, insurance activity, itssue growth activity, activin/inhibin activity.
                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1998.
10-APR-1998; U06956.
10-APR-1997; US-837312.
10-BRY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Racie LA, Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9845437-A2.
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V88129;
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17; Conser
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Pred. No.
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which would make
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7.1;
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                                                                                                                     (EST), and is the invention
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method comprised assessing genomic DNA from an individual for the 20 presence or absence of the HH-associated allele of the single base-pair 21 polymorphism HHP-1, HHP-19 or HHP-29, and/or at least one non-optional 22 marker comprising the following microsatellite repeat alleles of group 22 A and optionally of group B: 24B2, 2B8, 3321-1, 4073-1, 4440-1, 4440-2, 25 CC Group A: 19D9, 18B4, 1A2, 1E4, 24B2, 2B8, 3321-1, 4073-1, 4440-1, 4440-2, 25 CC Group B: 5091-1, 3216-1, 4072-2, 950-1, 950-2, 950-3, 950-4, 950-5, 950-6, 25 CC Group B: D63464, D65306, D65258, D65265, D65105 and D651001.

CC Group B: D63464, D65306, D65258, D65265, D65105 and D651001.

CC The absence of the genotype indicates the likelihood of the presence of the HH mutation of genotypes characteristic of heteroxygous carriers and 25 CC the HH mutation at the strength of the presence of 25 CC the head of the manual interferes with the effectiveness of interferon the constraint of the content of the cont
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Best Local S
Matches 17
Query Match

Best Local Similarity

Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using primers based on novel microsatellite repeat flanking sequences or on base-pair polymorphisms HHP-1, HHP-19 or HHP-29 Claim 24, Fig 1F, 67pp; English.

The sequences given in T72045-67 represent portions of the genome surrounding several markers of the invention. The markers were identified using the series of primer pairs given in T71973-2044 which were used to determine the presence or absence of the common the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of the common that is a series of the presence of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence flanking marker 950-2 in HH region of chromosome 6p2.1. primer; polymerase chain reaction; amplify, hereditary haemochromatosis; HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1; HHP-19; HLP-29; mlcrosatellite repeat allele; genetic marker; interferon treatment; hepatitis C infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERC-) MERCATOR GENETICS INC.
Drayna DT, Feder JN, Gnirke A,
Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1996; U06352.

08-MAY-1995; US-436074.

15-NOV-1995; US-559302.

09-FEB-1996; US-599252.
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                                                                                                                                                                    responsiveness
Sequence 688
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                                                                                                                                                                                                                                            treatment for hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 TCGGGAGGCCGAGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGGAGGCCGAGGCAG
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                                                                                                                                                                        interferon; 213 A;
                                6.2%;
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Pred. No.
                                                                                                                                                                 fection. By diagnosing this potential, treatment may be evaluated.
155 C; 137 G; 171 T;
                                Score 17;
Pred. No.
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7.1;
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7.1;
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                                                                   Length 688
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Conservative

Mismatches

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08-MAY-1996; U06583.

08-MAY-1995; US-436074.

15-NOV-1995; US-559302.

09-FEB-1996; US-599252.
14-MAY 1999 (LLIST COLOR)

DNA encoding a human secreted protein.

Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; developmental abnormality; foetal deficiency; developmental abnormality; developmental abnormali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A and optionally of group B:
Group A: 1909, 1884, 1A2, 1E4, 24E2, 2B8, 3321-1, 4073-1, 4440-1, 4440-2, 731-1, 5091-1, 3216-1, 4072-2, 950-2, 950-3, 950-4, 950-5, 950-6, 950-8, 63-1, 63-2, 63-3, 65-1, 65-2, 373-8, 373-29, 68-1, 241-6, 241-29; Group B: D6S464, D6S306, D6S258, D6S265, D6S105 and D6S1001. The absence of the genotype indicates the 11kelihood of the presence of the HH mutation. Knowledge of the new genetic markers allows the definition of genotypes characteristic of heterozygous carriers and homozygotes having a HH mutation in their genomic DNA. The potential for HH in an individual interferes with the effectiveness of interferon treatment for hepatitis C infection. By diagnosing this potential, the responsiveness of interferon treatment may be evaluated. Sequence 688 BP; 213 A; 155 C; 137 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing and genotyping of hereditary haemochromatosis (HH) using primers to detect specific polymorphisms of the HH gene on chromosome 6p2.1 or novel microsatellite markers
Claim 24; Fig 1P; 67pp; English.

The sequences given in T43925-55 represent portions of the genome surrounding several markers of the invention. The markers were identified using the series of primer pairs given in T71901-72
which were used to determine the presence or absence of the common hereditary haemochromatosis (HH) gene mutation in an individual. The method comprised assessing genomic DNA from an individual for the presence or absence of the HH-associated allele of the single base-pair polymorphism HHP-1, HHP-19 or HHP-29, and/or at least one non-optional marker comprising the following microsatellite repeat alleles of group A and optional to force the second compositional to force the second composition the following microsatellite repeat alleles of group and optional compositions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 GGGAGGCCGAGGCAGGA 274
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17; Conser
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                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                     DNA;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274
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                                                                                                                                                                                                                                                                                                     뫔
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in HH region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 688;
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RESULT
V11854
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                                                                                                                                                                                                                                                                                                           Proposition of pathalogical diseases

Proposition of pathalogical diseases

Provided human genes encoding secreted polypeptides - useful for provided human genes encoding secreted proteins and their corresponding continuations are described secreted proteins and their corresponding conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the secreted polypeptides in a sample or by determining the protein of conditions in the polynucleotides. Specific uses are described for each coff the products, based on which tissues they are most highly correspondent timours, neurodegenerative disorders, can disorders, can also foetal deficiencies, blood disorders, can disorders, can also foetal deficiencies, blood disorders, can be contained to the products for the disorders.
                                                                                                                                                                                                                       Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AUG-1997; US-056732.
05 AUG-1997; US-054798.
05 AUG-1997; US-054804.
05 AUG-1997; US-054806.
05 AUG-1997; US-054806.
05 AUG-1997; US-054808.
05 AUG-1997; US-054809.
05 AUG-1997; US-055310.
05 AUG-1997; US-055312.
05 AUG-1997; US-055312.
05 AUG-1997; US-055312.
05 AUG-1997; US-055386.
05 AUG-1997; US-055386.
05 AUG-1997; US-055386.
19 AUG-1997; US-055371.
18 AUG-1997; US-056365.
19 AUG-1997; US-056365.
19 AUG-1997; US-056371.
19 AUG-1997; US-0563731.
14-SEP-1998 (first entry)
Human Duffy genomic DNA se
Duffy gp-Fy; FY*B gene; bl
                                                      V11854 standard; DNA; 3523 BP V11854;
                                                                                                                                                        2199
                                                                                                                                                                                                                                                                                                     prostate diseases, asthma, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. Sequence 2351 BP; 702 A; 446 C; 518 G; 675 T;
                                                                                                                                                                                                                                                                                                                                                                                      diseases of the immune system, autoimmune diseases, hepatic and renal disease, diabetes, inflammation, allergies, ischemic shock, Alzheimer and cognitive disorders, schizophrenia, cardiovascular disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1997, US TO THE SCI INC. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens. W09907891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         renal disease; diabetes; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; cardiovascular disorder;
                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wer LA, Ebner R,
en HS, Rosen CA,
; 99-167452/14.
                                                                                                                                                                                     GGGAGGCCGAGGCAGGA 274
                                                                                                                                                                                                                        Similarity
17; Conserv
                                                                                                                                                                                                                       Conservative
ic DNA sequence (FY*B).
gene; blood group; blood typing; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrie AM
Ruben SM,
                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                        6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis; arthritis; ss.
                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greene
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'MĽ
                                                                                                                                                                                                                                      DB 1;
7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janat F,
Young PE,
                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                    Length 2351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9,4
                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's
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                                                                                                                                                                                                                       Gaps
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AC DT DT CKW KW PN PR PR PR
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V27017
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC (FY*B) used to produce transgenic mice. It was obtained by per CC amplification using FY-specific primers (see V11852-53). The CC amplified fragment was cloned in the pBluescript vector, and a CC purified DNA fragment containing the FY*B gene was microinjected CC into the male pronucleus of fertilised eggs of the B6/CBA F1'mouse. CC Transgenic mice were obtained. The invention relates to a method CC for making monoclonal antibodies (MAbs) having pre-defined CC specificity to an epitope characteristic of, or unique to, a single CC form of a polymorphic protein. This includes constructing a first CC transgenic animal to express a first form of a polymorphic protein cCC constructing a second transgenic animal to express a second form of constructing a second transgenic animal to express a second form of CC the polymorphic protein encoded by a second transgenic animal to induce an immune CC encoding the protein; and immunising the first transgenic animal considering the first transgenic animal to induce an immune CC response in the first transgenic animal to induce an immune CC response in the first transgenic animal to induce an immune CC polymorphic protein. The invention is particularly advantageous in the context of making MAbs and derivative reagents specifically CC identifying polymorphic blood group proteins, such as the Duffy CC qp-Fy protein.
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                   Homo sapiens DNA fragment containing FY*B coding sequence gp-FY protein; Fyb71-81; duffy blood group; antigen; alpha alternative splicing; RBC; red blood cell; malaria; treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods of producing antibodies specific for one form of a polymorphic protein - useful in blood typing etc.

Example 1; Fig 3A-B; 43pp; English.

This nucleotide sequence comprises a Duffy genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid ME;
WPI; 98-
14-NOV-1997; U21067.
15-NOV-1996; US-749543.
(NYBL-) NEW YORK BLOOD CENT INC.
                                                                       Homo sapiens.
WO9821224-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                        V27017;
                                                                                                                                                                                       V27017 standard; DNA; 3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1997; U20783.
15-NOV-1996; US-749527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                        11-SEP-1998
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                                                   22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NYBL-) NEW YORK BLOOD CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism; transgenic animal; hybridoma; monoclonal antibody;
                                                                                                                                                                                                                                                                              803 TTCTGGTCCCCACCTTT 819
                                                                                                                                                                                                                                                                                                              80 TTCTGGTCCCCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98-297923/26
                                                                                                                                                                                                                                                                                                                                                                                                                                   3523 BP;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "G
3501. .352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers complement (1. .23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "sense primer for DNA amplification"
1531. .2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                              6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3523
                                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                 720 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "antisense primer for DNA amplification"
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                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                              Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 1042 C;
                                                                                                     group; antigen; alpha; beta;
cell; malaria; treatment; ss
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 806 G;
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                               Length 3523;
                                                                                                                                                                                                                                                                                                                                                                                                                                 955 T;
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                                                                                                                                                                                                                                                                                                                                              Gaps
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Example 15; Fig 13: 87pp; English.

The sequence is that encoding a major subunit of the Duffy blood group antigenic system, the gp-Fy proteins. The gp-Fy proteins are gp-Fy alpha and gp-Fy beta which are produced from the same gene via a mRNA splicing mechanism. It contains the major receptor by which plasmodium vivax enters red blood cells (RBC) and causes malaria. The proteins are thus useful in preventing malaria and in regulating RBC, renal and neural function. The protein or certain fragments of it, may also be used to generate antibodies, complementary peptides and drugs modelled on their tertiary structure, useful in the same way. Sequence 3523 BP; 720 A; 1042 C; 806 G; 955 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaudhuri A, Pogo OA; wpr; 98-297854/26.
Nucleic acid encoding gp-Fy, Duffy antigen proteins - used to prevent vivax malaria and to regulate erythrocyte, neural or renal function
                                                                                          ty Match 6.2%; Score 17; DB 1; Length 3523; Local Similarity 100.0%; Pred. No. 7.4; ches 17; Conservative 0; Mismatches 0; Indels
80 TTCTGGTCCCCACCTTT 96
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Search completed: October 3, 2000, 14:37:36 Job time: 5195 sec

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Database :
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
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Human interleukin-
Bacterial artifici
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Human RAD54 nuclei
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Clone pTB1284 enco
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RESULT 2
Q95493/c
ID Q95493;
AC Q95493;
BY 21-NOV-1995 (first entry)
BE Human Cdn-2 DNA.
KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
KW shock; lymphoma; eczema; ss.
OS Homo sapiens.
Location/Qualifiers
FT cds 3312..3947
FT cds 3312..3947
FM W09515084-A.

B 8

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Query Match Best Local Matches 2	PT New isol PS Claim 2; CC This seq CC to expre CC genes (c CC represse (c CC penes (c CC be used CC also be CC dassociat CC associat CC be used SQ Sequence	394	33 3 3 4 4 4 4 3 3 4 4 4 3 3 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Simi 6;	Claim 2; Page 143-147; 184pp; Claim 2; Page 143-147; 184pp; This sequence represents a hu to express by both HCMV and if genes (cig or cigs). The invert repressed in the presence of legens (crg or crgs). The produce used for anti-viral theraph also be used for the development of	1999 1099 1099 1000 1000 1000 1000 1000	222222222222222222222222222222222222222
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vat	agé human genes sige 143-147; 184pp; nce represents a hu by both HCMV and i or cigs). The invei in the presence of i or crgs). The prod c anti-viral therap; ad for the developme treatments without with administering r detection, diagno; 3200 BP; 972 A;		240 240 240 240 240 240 260 260 260 260 260 260 260 260 260 26
ф·	184pp; Ensist a human interior and interior end interior		
Score 26; DB 1; L Pred. No. 0.00019; 0; Mismatches 0;	English. man gene of the state	entry) entry) e gene, SEQ ID NO 21. cig; human; human cytomegalovirus; interferon; anti-HCMV therapy; detection; diagnosis; 725. 180. TON. hu H;	T17519 T17521 T17522 T17523 T17524 T17526 T17526 T17528 T17529 T17529 T17529 T17529 T17520
Length 3200; 019; 0; Indels	the invention, that is islates to genes that a n, designated HCMV-re used to obtain agents that a still the thing that a nit. HCMV therapy. That would allow for that would allow for if IFN. The products screening.	igalovirus; inte ion; diagnosis;	Mutate
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RESULT
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY IN BAIT PJ. Kiefer MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acta with Cdn-1 (R77876).

Sequence 6511 RD.
            is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                    Claim 1; Page 1942; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAS. Each library
                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene signature HUMGS08078.
Gene signature; messenger RNA; mRNA;
human; cloning; mapping; non-biased l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T25848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barr PJ, Kiefer M
WPI; 95-215106/28.
P-PSDB; R77877.
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                                                                                                                                                                                                                                                                  tissues
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12-NOV-1993; JP-355504
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Pred. No.
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library; diagnosis; detection;
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0.0022;
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                                                                                          of.
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Query Match Best Local Similarity

6.6%;

Score Pred.

23; No.

> DB 1; 0.0064;

Length

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RESULT 4
V39298/c
ID V39298 standard: c
AC V39298;
DT 16-SEP-1998 (firs
DE Human RAD54 nuclei
KW Human; RAD54; hRAD
KW Werner's syndrome;
KW Y-linked mental re-
CO Samplens.
PN EP-844305-A2.
PN EP-844305-A2.
PN EP-844305-A2.
PN EP-844305-A2.
PN EP-84305-A2.
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ACC DET DE KW KW PN PN PR PR
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Best Local Similarity

Matches 22: Conservations
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EP-844305-A2.
27-MAY-1998.
10-NOV-1997; 308998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present in tumours that display allelic imbalance at 1732, the chromosomal band identified as one of four minimal regions of chromosome 1 deletion in breast carcinomas. hRAD54 is useful for production of proteins, inter alia, that have been identified as novel hRAD54 homology between the amino acid sequence given in W62186 and known amino acid sequences such as yeast RAD54. hRAD54 proteins are used in the treatment of cancer, including Xeroderma Pigmentosum and Bloom syndrome, Werner's syndromes and X-linked mental retardation with alpha-thalassaemia syndrome and
                                                                                                                                                                                               Lung cancer specific antigen HCAVIII promoter region genomic, Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII; carbonic anhydrase; diagnosis; therapy; promoter; DNA probe; fluorescent in situ hybridisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                         T15455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T15455 standard; DNA; 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer. hRAD54 polynucleotides are also useful for detecting complementary nucleotides for use as a diagnostic agent, especially useful for diagnosis of disease or susceptibility to diseases. hRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
(UYJE-) UNIV JEFFERSON THOMAS.
CTOCCE CM, Fishel RA, Rasio D, Robbins DJ;
WPI: 98-274189/25.
                                                                                  01-FEB-1996.
                                                                                                                          WO9602552-A1.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide, proteins, agonists and antagonists which are proteins are useful in gene therapy.

Sequence 840 BP; 190 A; 200 C; 221 G; 229 T; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a specifically claimed partial acid sequence encoding human RAD54 (hRAD54). A method for analysample for mutation of DNA encoding hRAD54 has been developed to the contract of the contract of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrowerner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumo
19-JUL-1995;
19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 28; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 CAGGAGTTCCAGACCAGCCTGG
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PP PR 311 PP PR 114 PP PR 116 PP PR 27 PP PR 116 PP PR 27 PP PR 116 PP PR 27 PP PR 2
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27-APR-1990; JF-113146.
31-JUL-1990; JF-204438.
14-SEP-1990; JP-24556.
28-DEC-1990; JP-415801.
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                                                                                                                                                                                                                                                                                                                                            New mutchin(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 8; 88pp; English.

A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1228 (see 014848). The complete FGF coding sequence was obtained by ligating the insert from pTB1228 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from
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Q14851;
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A genomic clone (T15455) was isolated that constitutes the putative promoter of the HCAVIII gene (see T15448), and probably contains transcription regulatory elements directly implicated in expression of HCAVIII, a cell surface antigen which is highly specific for non-small cell lung carcinoma and which has features in common with human carbonic anhydrases. The clone was obtd. by PCR amplification using a primer pair (T15456-57) based on the putative exon 6 of the HCAVIII gene. A DNA probe comprising the genomic clone plus flanking sequences was used for fluorescent in situ hybridisation. Sequence 1363 BP; 352 A; 382 C; 369 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEMICAL IND KK. Igarashi K, Senoo M, Watanabe T; WPI; 91-353723/48.
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Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer specific antigen HCAVIII
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New mutein(s)
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Bollon AP, Torczynski RM;
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14-N0V-1991, J00557.
25-APR-1990, JP-113146.
27-APR-1990, JP-204438.
14-SEP-1990, JP-245256.
28-DEC-1990, JP-415801.
(TAKE) TAKEDA CHEMICAL I
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A cDNA library prepared from human cancer cell line Kato III mRNA a cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1229 (see 014849). The complete FGF coding sequence was obtained by ligating the insert from pTB1229 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from the complete FGF coding sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from
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3203. .3386
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Pred. No.
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Mismatches

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Best Local
 W09315196-A
                                                                                                                                                                                                                                                                                                                                                                                                          human alpha-N-acetylglucosaminidase (W18017), an enzyme that can hydrolyse the terminal alpha-N-acetylglucosamine residues at the non-reducing terminus of fragments of heparan sulphate and heparin. It was isolated by hybridaisation of a human chromosome 17 library. A cDNA clone (T67163) coding for the enzyme has also been isolated. The isolated gene or cDNA, and primers/probes based on them or their complementary strands, can be used to investigate, diagnose and treat alpha-N-acetylglucosaminidase deficiency, for example in patients suffering from mucopolysaccharidosis type IIIB.

Administration is by oral, i.v., i.p., enzyme replacement therapy,
                                                                                                                   exon
                                                                                                                                                                                                              Q46852 standard; DNA; 13104
Q46852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding mammalian alpha-N-acetylglucosaminidase used for the diagnosis and treatment of mucopolysaccharidosis type IIIB, also used in gene therapy Claim 8; Page 54-61; 79pp; English.

A genomic DNA molecule (T67164) includes 6 exons that code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1996; AU0747
23-NOV-1995; AU-006748.
(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Anson DS, Blanch L, Hopwood JJ, Sco
WPI; 97-298114/27.
                                                                                                                                                                         Clone of recombinant human kappa casein gene fragment. Casein; supplement; milk; pharmaceutical; ss.
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                  26-JAN-1994 (first entry)
                                                                                                                                                                                                                                                                                   7439 CAGGAGTTCCAGACCAGCCTGG 7418
                                                                                                                                                                                                                                                                                                                                                                                       gene therapy or other routes. Sequence 10380 BP; 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W18017
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/number= 4
3473. F
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7745. .8955
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10511.
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10015.
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5667. .
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12278.
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                                                                                          .10014
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                       .12443
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Pred. No.
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                                                                                                                                                                                                                                                                                                                               Mismatches
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0.025;
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RESULT T71699
ID T71899
ID T71
AC T71
DT 20--
DE Hum
PN US5
PD 10--
PR 10--
PR 10--
PR 10--
PR 10--
PR 10--
PR WP1
DR WP1
DR WP1
CC The
CC The
CC 196
CC 196
CC 196
CC The
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T71696
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Best Local S
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Best Local S
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T71696 standard; DNA; 26764
T71696;
20-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the human deoxycytidylate (dCMP) deaminase intron 2, which comprises 20303 base pairs from nucleotides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant deaminase
Claim 2; Column 83-100; 58pp; English.
The present sequence encodes the huna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T71byy;
20-AUG-1997 (first entry)
Human deoxycytidylate deaminase
Human deoxycytidylate deaminase;
dCMP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T71699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The recombinant human Kappa casein is produced in high yields by means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. [It can also be used as a pharmaceutical.

Sequence 13104 BP; 4256 A; 2497 C; 2397 G; 3953 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HEAL-) HEALTH RES INC.
Maley F, Maley GR, Weiner KXB;
WPI; 97-244391/22.
DNA encoding human deoxycytidylate deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
US5622851-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-AUG-1993.
25-JAN-1993; DK00024.
23-JAN-1992; DK-000088.
(SYMB-) SYMBICOM AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             to mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1995; 370975.
10-JAN-1995; US-370975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide(s) for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human kappa-casein - used for obtaining recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bergstroem S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1997.
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                                                                                                                                                                                                                   289 CAGGAGTTCCAGACCAGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   removed or mutated) to alter DNA replication in cells, which may lead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 CAGGAGTTCCAGACCAGCCTGG 306
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                                                                                                                                                                                          CAGGAGTTCCAGACCAGCCTGG
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22; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20303 BP;
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 5454 A;
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                                                         ВP
                                                                                                                                                                                          15305
                                                                                                                                                                                                                                            310
                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                            Score :
Pred.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 5052 G;
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deoxycytidylate deaminase

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                                    V20441/c
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                                                                                                          Query Match
Best Local Similarity
Matches 22; Conser
                                                                      Claim 3; Column 55-78; 58pp; English.

Claim 3; Column 55-78; 58pp; English.

The present sequence encodes the human deoxycytidylate (dCMP) deaminase gene, which contains a 5' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to Also, the dCMP gene can be altered (removed or mutated) to alter replication in cells, which may lead to mutagenesis.

Sequence 26764 BP; 7079 A; 5521 C; 6539 G; 7625 T;
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                 V20441 :
V20441;
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Human c-fms oncogene
                                                                                                                                                                                                                                              DNA encoding human deoxycytidylate deaminase - recombinant deaminase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                    LO-JAN-1995;
LO-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iomo sapiens
                          standard; DNA; 35100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deaminase; dCMP;
                                                                                                            Conservative
       (first entry)
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                                                                                                                                                                                                                                                                                                              370975
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25392. .:
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23741. .:
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/number= 1
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1. .1317
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1964. .22266
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*tag= f
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                                                                                                                    Score 22;
Pred. No.
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                                                                                                            Mismatches
                                                                                                                     DB 1;
0.026;
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                                                                                                                              Length 26764;
                                                                                                                                                                                                                                                       production
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US5734039-A.
31-MAR-1998.
15-SEP-1994; 306691.
15-SEP-1994; US-306691.
(UVJE-) UNIV JEFFERSON THOMAS.
human chromosome 10, 10925.2 region. The sequence in unusual chromosomal marker referred to as mardel(10). The an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional neocentromere at a location regarded as non-centromeric. This neocentromere maps to 925.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33551 CAGGAGTTCCAGACCAGCCTGG 33530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLI/MTGB, E2A/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 59-90; 92pp; English.
The present sequence represents an oncogene from the present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for general contents of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NC-contig derived from mardel(10) on chromosome 10q25.2. Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; recent control carbination; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calabretta B, Skorski T; WPI; 98-229882/20.
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cancer; antisense oligonucleotide; c-fms; ds.
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the NC-contig derived from a human chromosome 10, 10q25.2 region. The sequence contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 16A; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancilla MR, Choo K, WPI; 99-009773/01.
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13-MAY-1998; AU0352.
26-AUG-1997; AU-008791.
13-MAY-1997; AU-00784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anticancer composition comprising two anti-sense oligo:nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
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03-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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0.026;
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W09851790-A1.

19-NOV-1998.

13-MAY-1998; AU0352.

26-AUG-1997; AU-008791.

13-MAY-1997; AU-006784.
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                                                                                                                                                                                                                                                                                   necentromere at a location regarded as non-centromeric. This peocentromere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80240 BP; 23102 A; 16537 C; 16747 G; 23846 T;
                                                                                                                                                                                                 expression of cytokines, receptors and growth factors, or to income the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.

Sequence 80595 BP; 23183 A; 16613 C; 16824 G; 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the HC-contig derived from normal human chromosome 10, 10q25.2 region. This region can be naturally mutated to produce an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; marchel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMRA-) AMRAD OPERATIONS PTY LTD. Cancilla MR, Choo K, Du Sart D; WPI; 99-009773/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-1999 (first entry)
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CAGGAGTTCCAGACCAGCCTGG
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Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species; almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of distraction as a means of distraction as a means of distraction and probes derived from the GS sequences) as a means of distraction as a means of distraction and probes derived from the GS sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determined (esp. using primers and process) as a means of diagnosing abnormal cell function recognising different cell types.

Segmence 158 BP; 46 A; 35 C; 44 G; 30 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                    258 GGGAGGCCGAGGCAGGAAGAT 278
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Gapop 60.0 , Gapext 60.0
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1 GCAAACAGAGCGCCACTGGG.....TACTTTGAAACATCTACTGG 205
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                                                                                                                                                                                                                                                                              Score
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gb_htg16:*
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AC018744
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AC010429

AP000817

AC022414

AC023220

AP001795

AC021203

AC021203

AC011640

AC021986

AC024177
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U95626 Homo sapien
AC018744 Oryza sat
AL121928 Homo sapi
M23166 S.cerevisia
10812 Sequence 1
109397 Sequence 5
X15135 Yeast NAT 1
Z74088 S.cerevisia
Z71781 S.cerevisia
Z71781 S.cerevisia
AL034563 S.pombe c
AC022747 Homo sapi
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AC023210 Homo sapi
AC013210 Homo sapi
AC011021 Homo sapi

Description

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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JOURNAL
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Unpublished (1997)

(bases I to 143068)

CCombie,R.W., Wilson,R., Chen,E., Gibbs,R., Zuo,L., Johnson,D.,
McCombie,R.W., Wilson,R., Chen,E., Mardis,E., Schutz,K.,
Nhan,M., Parnell,L., Dedhla,N., Anghan,N., Greco,T., Tuochman,J.,
Gnoj,L., de la Bastide,M., Kaplan,N., Greco,T., Tuochman,J.,
Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M.,
Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M.,
Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M.,
Sollnsky,K.A., Dassilva,U., Diaz-Perez,S., Zhou,X., Yu,Y.,
Sollnsky,K.A., DeSilva,U., Diaz-Perez,S., Zhou,X., Yu,Y.,
Sollnsky,K.A., DeSilva,U., García,D. and Sagripanti,J.-L.
                                                                                                                                                                                                                                   Cold Spr
NY: 11724
Regions
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Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.
Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.
Direct Submission
Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course,
Submitted (27-MAR-1997) Advanced Genome Rd., Cold Spring Harbor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCombie, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Mhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L. Human BAC clone 110P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens ccr2b (ccr2), ccr2a (ccr6) genes, complete cds, and l partial cds, complete sequence 095626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates; Ca
1 (bases 1 to 143068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ccr2a (ccr2), ccr5 (ccr5) and ccr6
and lactoferrin (lactoferrin) gene,
                                                                                                                             53303 -
65200 -
112377 -
134914 -
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AF055992 Homo sapi
U43899 Human signa
S76830 glycoprotei
AE001168 Borrelia
AC014464 Drosophil
AF077546 Caenorhab
AP001049 Homo sapi
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X96440 E.chrysanth
AK001422 Homo sapi
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gene

mRNA

Sdo

Harbor,

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AC018744 216514 bp DNA Oryza sativa chromosome 10 clone 15022,
                                                                                                                                                                               9.3%; Score 19;
Similarity 100.0%; Pred. No.
19; Conservative 0; Mismatc
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127884 ...128068, 330006 ...130073,13203 ...132164,
133863 ...134018, 135022 ...135075, 115890 ...13590,
137445 ...137599, 138436 ...138610,139077 ...>139253))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"confirmed by similarity to lactoferrin mRNA, accession number M73700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(124605 .124816,126528 .126717, 127884 .128068,130006 .130073,132023 .132164, 138863 .134018,135022 .135075,135890 .135980, 137445 .137599,138436 .138610,139077 .>139255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"confirmed by similarity to lactoferrin protein, encoded by GenBank Accession Number M73700, gi 186818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(124605. .>139255)
/gene="lactoferrin"
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Translated sequence exhibits 42% sequence identity to CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Putative mRNA identified by homology to CCR5 mRNA."
/product="ccr6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="lactoferrin"
/protein_id="AAB57795.1"
/db_xref="GI:2104522"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"ccr6"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                    Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC018744.2 GI:7191023
HTG; HTGS_PHASE1.
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1 (bases 1 to 216514)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n Mar 7, 2000 this sequence version replaced gi:6730690.

NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                      Conservative
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/db_xref="taxon:4530"
/chromosome="10"
/clone="15022"
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                    9.3%; Score 19; DB
100.0%; Pred. No. 4.7
tive 0; Mismatches
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ig of 3800 bp in length
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Insert size: 164357; 5.4% error; agarose-fp
Quality coverage: 6.37x in Q20 bases; sum-of-contigs Quality
coverage: 8.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSBA18I14 225415 bp DNA HTG Homo sapiens chromosome 10 clone RP11-18I14, PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Informatio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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(bases 1 to 225415)
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Eutheria; Primates;
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184902
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fragment_chain:3"
106752...142041
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73292. .7
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fragment_chain:3"
142142. .153747
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68973. .71980
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/db_xref="taxon:9606"
/chromosome="10"
                                                                    fragment_chain:
                                                                                                                          /note="assembly_fragment:04188
fragment_chain:3"
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75769. .10665
          /note="assembly_fragment:03147
fragment_chain:4"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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206684. .208153
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216578. .217599
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213397. .21498
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                  Sequence 1 from Patent 108122
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Molecular cloning and sequencing of a cDNA encoding N alpha-acetyltransferase from Saccharomyces cerevisiae
J. Biol. Chem. 264 (21), 12339-12343 (1989)
                                                                                                                                                                                                                                          th 8.8%; Score 18; DB Similarity 100.0%; Pred. No. 27 18; Conservative 0; Mismatches
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QFEDDQLDFHSYCMRKGTPARJKENLEWKEMYVRAMKEASKLYVQMHDDRLK
RKSDSLDENSDEIQNNGQNGSSQKKKAKKEAAMNKRKETEAKSVAAYPSDQDNDVFE
EKLIETSTPMEDFATEFYNNYSMQVREDERDYILDFEENYRIGKLALCEASLNKEAKR
FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDWL
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HFLFLKDFPKAQEYIDAALDHTPTLVEFYILKARILKHLGLMDTAAGILEEGRQLDLQ
DRFINCKTYKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASWFIVEQAEAYY
  GI:589163
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NWTSLAVAQDVNGERQQAINTLSQFEKLAEGKISDSKYEHSECLMYKNDIMYKAASD
NODKLQNVLKHLNDIEPCVFDKFGLLERKATIYMKLGQLKDASIVYRTILKRNFDNFK
YKLLEVSLGIQGDNKLKKALYGKLEQFYPRCEPPKFIPLTFLQDKEELSKKLREYVL
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/strain="TD71.8"
/db_xref="taxon:4932"
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AILKKDGSHVDSLALKGLDLYSVGEKDDAASYVANAIRKIEGASASPICCHVLGIYMR
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/protein_id="AAA88728.1"
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/note="(vector lambda gtll)"
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                                                                       baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 3347)
                                                                                                                                                              SCNAT 3347 bp DNA PLN Yeast NAT 1 gene for N-terminal acetyltransferase. X15135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolation, purification, characteriz of N alpha-acetyltransferase Patent: EP 0334004-A1 1 27-SEP-1989; Location/Qualifiers 1. .2699
                                 Direct Submission
Submitted (27-APR-1989)
Angeles CA 90024, USA
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 2724)
Smith,J.A. and Lee,F-J.S.
Patent: Wo 8907138-A 5 10-AUG-1989;
Location/Qualifiers
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          Mullen,J.R.,
                                                                   Grunstein, M
                                                                                                                                        acetyltransferase; NAT 1
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Smith, J.A. and Lee, F-J.S.
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Kayne, P.S., Moerschell, R.P., Colavito-Shepanski, M., Grunst
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                                             Grunstein M., UCLA, Biology Department,
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Direct Submission
Submitted (09-JUL-1996) Data collected by MIPS on behalf the project of the submitted project. MIPS are suppean yeast chromosome IV sequencing project. MIPS Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
1. ,3530
                                                                                                                                                                                                        Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3530)
Paulin,L., Saren,A.M. and Laamanen,P.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                               SCYDL040C 3530 bp
S.cerevisiae chromosome
274088 271256
274088.1 GI:1431024
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Identification and characterization of genes and w-+arminal acetyltransferase from yeast
                                                                                                                                                                                                                                                                                                                                                         baker's yeast.
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Location/Qualifiers
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NYMSLAVAQDVNGEROQAINTLSQFEKLAEGKISDSEKEHSECLMYKNDIMYKAASD
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YYKLLEVSLGGIQGDNKLKKALYGKLEOFY PRCESPKIPLIFLQOKEELSKKLREVYL
PQLERGVPATESNVKPLYQRRKSKVSPLLEKTVLDYLSGLDFTQDPIOPI PFTWTNYYLSQ
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DRFINCKTVXYFLAANNIDKAATEVASLFTKNDDSVNGIKDLHLVARSWFIYGAAEAYY
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RKSDSLDENSDEIQNIGQMSSSQKKAKKREAAAMNKRETEAKSYAAYPSDDDINYVFG
EKLLETSTEMEDFATEFYNNYSMOVERDERDYILDFENNYRIGKLACFASLNKFAKR
RKSDSLDENSDEIQNIGQMSSSGOKKAKKEAAAMNKRETEAKSYAAYPSDDDINYFG
EKLLETSTEMEDFATEFYNNYSMOVERDERDYILDFENNYRIGKLACFASLNKFAKR
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/db_xref="taxon:4932"
337. 2901
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/db_xref="GI:578200"
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IV reading frame ORF YDL040c
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                                                                                                                                                                                                                                                   Saren,A.M., Laamanen,P., Lejarcegui,J.B. and Paulin,L. The sequence of a 36.7 kb segment on the left arm of chromosome from Saccharomyces cerevisiae reveals 20 non-overlapping open reading frames (ORFs) including SIT4, FAD1, NAM1, RNA11, SIR2, NAT1, PRP9, ACT2 and MPS1 and 11 new ORFs
                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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act2 gene; actin; FAD synthetase; FAD1 gene; MPS1 gene; NAM1 gene;
NAT 1 gene; protein kinase; protein phosphatase; SIR2 gene; SIT4
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Z71781
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18; Conserv
                                                                                       Submitted (23-APR-1996) Paulin L., Institute of Biotechnology, DNA sequencing & Synthesis Laboratory, Biocentre 1, P.O.BOX 56 (Viikinkaari 9), FIN-00014 University of Helsinki, Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               baker's yeast.
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ilarity 100.0%;
Conservative
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RKSDSLDENSDEIQNNGONSSSOKKRAKKEAAAANNKREFTEAKSYAAYSDODNNYFG
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FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDML
NFYQEKFGKNDINGLLFLYRYRDDVPIGSSNLKEMIISSLSPLEPHSQNEILQYYL"
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complement(419. .2983)
                                              1. .36687
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/organism-"Saccharomyces cerevisiae"
/strain-"alpha S288c"
                                                                 Location/Qualifiers
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LCVHGGLSPEIRMLDQIRTLSRAQEVHEGGESDLLMSDPDNVEAWQVSFGAGWHEG
SKVAREENHYNGLNLIARAHQLVMEGFKYHFPEKDVTVWSAPNYCYRCGNVASVMKV
DEDLEPTFKIFSAVPDDYIRESTANHNNQRAGYFL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"chromosome library of C. Jacq (Paris)"
complement(<1. .556)</pre>
complement(6581. .7630)
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                                                                                                                         complement(6581. .7630)
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ITCLTGEVIFPPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="protein phosphatase catalytic subunit homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Protein sequence is in translation; Acc.no. X01419"
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Best Local S
Matches 18
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fission yeast.
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales,
Schizosaccharomycetaceae; Schizosaccharomyces.
1 (bases 1 to 43325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-phosphogluconate dehydrogenase decarboxylating; cell wall protein; class v pyridoxal phosphate dependent aminotransferase; elongation factor g; elongation factor Tu family; fbpl; fructose-1,6-bisphosphatase; 6 beta repeat; glycine-rich protein; low-complexity gene-free region; mikl; mitosis inhibitor protein kinase mikl; myb like dna-binding protein; neutral trehalase; ntpl; polya-binding protein; rasll; replication factor a protein 1; polya-binding protein; RNA recognition; RNA3' Cleavage factor Ib; rpal; ssbl; transcription initiation factor iif beta subunit; WD domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                          (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome
sequenced by the Sanger Centre. The sequencing of th
genome is now being continued with funding from The E
                                                                                                                                                                                                                                                                                                              sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and Biotechnologische und molekularbiologische Forschung, angelhofweg 39, D-69259 Wilhelmsfeld, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyne,M., Rajandream,M.A., Barrell,B.G. and Rieger,M. Direct Submission Submitted (18-DEC-1998) European Schizosaccharomyces
Commission. Fourteen European sequencing laboratories, the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with
                                                                                                                                                                                                                                                 Details of yeast sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yeast CF Ib.
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                                                                                                                                                                                                                    the world wide web.
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complement (14327. . . 14674)
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pred. No. 19;
mismatches
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. 19;
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                                                                                                                             the S. pombe
                                                                                          European
                                                                                                                                                                                                                                                    available
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                                                                   including
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FEATURES
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                                   Sg
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The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c660 is overlapped at the 3' end by cosmid 1198 (contained in EMBL entry SP33010 accession number U33010).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splice donor/acceptor sites.
CDS are numbered using the following system eg
pombe), B (chromosome 2), c25H2 (cosmid name),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                computer analysis using the Genefinder program in PomBase (an ACED) database) with additional predictions for the branch-acceptor sites supplied by the program 5935plice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number of introns/exons or we may not have chosen the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (complementary strand).
                                                                                                                                                                                                                                                                                                                                                                        /note="gtaagt, splice donor sequence" complement(join(383..464,506..537))
/gene="SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pombe chromosome 2" complement(87. .104) /gene="SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdtsvinpelqihgfigvdslqssrkkndeddfplnkglktnn ndysgslepkispalsikedgkndrneralmslagdsplnksgletsia ndysgslepkispalsikedgkndrneralmslagdsplnkseri shedbilasssia lgndnudssallskulkglesilispseltinmdfelkgsarwtaeh wdylerrmonrovsluhtovadsliekkrligplsslvkllvgemfsftrfilthl ralynipgyekysfrknsgkdegvoetaiisoevhneimdogwseyofcnoiwagkc pkiirmfysnlykklshadakslyhyrdaynfedrowskedbeelknnvoehgkc wtkigkkmarmbuckdrbakslyhyradynfeddkolywskedbeelknnvoehgkc wtkigkkarmambuckdrbakslyhyradynfedlkolybbelknnablssd inwilvadmlogyrtrockfolykkaskfeldenvwlleriydsllnnggkihwe invkeangkwitho"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SPBC660.01c, SIMILARITY:Schizosaccharomyces pombe, CAB52717, putative myb-like dna-binding protein, (496 aa), fasta scores: opt: 478, E():4.7e-23, (30.6% identity in 350 aa)"
                                                                                                                                                     /note="ttaacgtttag, s
complement(500..505)
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                                                                                                                                                                                                                                            DNA-binding domain Score complement(465. .475)
//gene="SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ctaatattttaattttaag, splice branch
complement(132, .137)
/gene="spbc660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative myb like dna-binding protein"
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DNA-binding domain_score 30.86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="nominal overlap with cosmids
oombe chromosome 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPBC660.01c"
/note="SPBC660.01c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1. .1482)
/gene="SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome="II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Schizosaccharomyces pombe"
/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="SPTREMBL:094422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-SPBC660.01c
                                                                /gene="SPBC660.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="cosmid c660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lement(join(1. .86,138. .464,506. .1482))
                                                                                                                        tatgt, splice donor sequence
                                                                                                                                                                                                                      splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP33010, EM:U33010 S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACEDB
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misc_feature
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                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPBC660.02"
/gene="SPBC660.02"
/note="Match to PF00400 WD40, W
Score 31.68"
3771. 3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461, E():2.9e-32, (31.0% identity in 368 aa); SPBC660.03c, len:307, SIMILARITY:Saccharomyces cerevisiae, T2FB_YEAST, transcription initiation factor iif, beta subunit, (400 aa), fasta scores: opt: 461, E():1.4e-22, (31.0% identity in 368 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(3930. .4184,4288. .4431,4491. .5015))
/gene_"SPBC660.03c"
/note="SPBC660.03c, len:307, SIMILARITY:Saccharomyces
/cerev isiae, YGR005C, T2FB_YEAST, transcription initia
factor iif, beta subunit, (400 aa), fasta scores: opti
461, E():2. 9e-32, (31.0% identity in 368 aa);
                        /note="ctaacttttttttcag,
complement(4485 .4490)
/gene="SPBC660.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYRSSRPLHKFEEHTAAVKAIGWSPHQRGILASGGGTIDRCLTIHNTLTGRLQNKLDT
GSQVCNMAWSKTSNEIVTTHGFAKNQVSLWKYPSLKNIANLTAHTNRVLYLSMSPDGQ
SIVTGAGDETLRFWKLFNKKPKEESTLIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="Sptrembl:094423"
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QKPKRAFPKTPYKILDAPYLKNDFYLNLLDWGQSNVLAVGLASSIYLWSAASGKVVQL
                                                                                                                                /note="gtatgt, splice donor
complement(4432. .4447)
                                                                                                                                                                                                         /note="ctaatgaattcatattag, complement(4282..4287)
                                                                                                                                                                                                                                                                                                                 VKQPEVYLKEVLDSIAILNKRGPYALKYSLKPEYKGTMDAASVELRNQQASQSESSSI
DHTGKNTSPDNPGTNAEEDEDDDGVEMIDVV"
                                                                                                                                                                                                                                                                                                                                                                  /translation="MSEEKPTVRTEEDDRYEDDAGDLDLGQIGSRVWLVKIPKFLMDK
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TSSSMKSTALVGTVAHECNUSSVINDDYRRVMQKRALASAPKRKVQMLDDRGGSLA
PGTLGSRSRSTTSFIRNVKPRTGEGLKNSRIPRNELLDILFKCFEDYEVMTLKGLREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="gtatgt, splice 2772. .2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDFGATNHVTSVLWTGKGTQLAVGTDSGVIYIWDIESTKSVRSLKGHSERVAALAWND
NTLTSGGKDEVILHHDLRAPGCCAEMMKVHEQEICGLQWDRSLGQLASGGNDNNLFVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SPBC660.02, len:421, SIMILARITY:Schizosaccharomyces
pombe, 013286, srwl., (556 aa), fasta scores: opt: 1364,
E():0, (50.6% identity in 385 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPBC660.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPBC660.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPBC660.02"
                                                                                                                                                                                                                                                             /gene="SPBC660.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/product="transcription initiation factor iif, beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Match to PF00400 WD40,
score 20.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SPBC660.02"
/note="Match to PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPBC660.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="ctaacgacagcag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SPTREMBL:094424"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GI:404950]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to PF00400 WD40, WD domain,
splice donor sequence"
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.1"
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                                                                            splice branch and acceptor"
                                                                                                                                                                                                                                       splice branch
                                                                                                                                                        sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain,
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                                                                                                                                                                                                                                       and
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AUTHORS
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AUTHORS
TITLE
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ORGANISM
                                                                                                                                                                                                    COMMENT
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VERSION
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AC022747/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
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                                                                                                                                                                                                                                                                                                Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marguis, N., McDwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A., and Zody, M.
                                                                                                                                                                                                               Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center
Submitted (06-FEB-2000) Whitehead Institute/MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhin1; HUNLALLE, Eutheria; Primates; Catarrhin1; HUNLALLE, Eutheria; Primates; Catarrhin1; HUNLALLE, Eutheria; Francisco (Catarrhin1; HUNLALLE, Eutheria; Francisco (Catarrhin1; HUNLALLE, Eutheria; HUNLALLE, Eutheria; Francisco (Catarrhin1; HUNLALLE, Eutheria; HUNLA
                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                 earch, 320 Charles Street, Cambridge, MA 021
repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
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                                                            Center code: WIBR
                                                                                Center: Whitehead Institute/ MIT Center for Genome
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                               site: http://www-seq.wi.mit.edu
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/product="fructose-1,6-bisphosphatase"
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sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                              represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 0073 length: 7736bp Contig_ID: 0073 Length: 17572bp Contig_ID: 00923 Length: 76087bp.
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence will the preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests:
On Apr 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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Homo sapiens chromosome 6 clone RP1-278E11,
PROGRESS ***, 3 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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26109 26508: gap of 800 bp
26909 102995: contig of 76087 bp in length
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/db_xref="taxon:9606"
/chromosome="6"
                                          /clone="RP1-278E11"
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                                                                                                                                                                                                                                                                                                                                                                                            The true right end of clone 206D15 is at 104. The true right end of clone 86F14 is at 106571. 86F14 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JAN-1998) Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 13, 1998 this sequence version replaced gi:2578147. IMPORTANT: This sequence is not the entire insert of clone 86F14. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS86F14 106571 bp
Human DNA sequence from
coagulation factor V, ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neighbouring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lq23-lq24; blood coagulation factor;
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                       .1858
/note="MLTIE
1876..27'
                                                                                                                        /note="N
1410. .1
                                                                                                                                                                                                          810.
                                                                             /note-"MLT1D
1575. .1858
                                                                                                                                                                                                                                                                 /map-"1
                                                                                                                                                                 /note="AluSx repeat:
1270. .1360
                                                                                                                                                                                                                                                  /map="1q23-1q24"
/clone="RP1-86F14"
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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100.0%; Pred. No.
                                                                                                                        "MLT1E repeat: .1587
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m PAC 86F14 on c
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                                                            265.
                                                                                                  139.
                     921.
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                                                                                                                                           .84 of consensus"
                                                                                                                                                                                      .302 of
                                                                                                  .323 of consensus"
                   .1 of
                                                            .568 of consensus
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                   consensus "
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4.7
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/note-"match: multiple ESTs; match: R71060 H69028 R82016 R10102 R82280 R82281; match: R82066 H69792 H79486 AA506861 T78091; match: W03874 H74282 D85229" Complement(join(27431 .27577,28562. 28744,31530. .31681,33638 .33782,36315 .36470,36919 .37022,37955 .38026,39019 .39135,41033 .41212,42726 .42936,43904 .44140,49624 .49798,53412 .56232,57414 .57626,59560 .59710,62919 .63133,63758 .63857,65675 .65852,68300 .68465,69764 .69985,72271 .72414,73672 .73884,85339 .85461,95549 .95640,99347 .99504))
                                                                                                                                                                                                                                                                                                                                                                   /note="L1MA7 repeat: matches 1017. .895 of consensus" 27046. .>27579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <25068. .25543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1MB4 repeat: matches 797. .902 of consensus" 22748. .22851
/note="L1MB5 repeat: matches 812. .922 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSc repeat: 3877. .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1 repeat: matches 5390. 2854. .3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches complement(10749. .11106) /note="match: STS G05144" 11725. .12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1 repeat: matches 3338.
19683. .20571
/db_xref="SPTREMBL:043737"
/translation="MFPGCPRLWVLVVLGTSWVGWGSQGTEAAQLRQFYVAAQGISWS
/RPEPTNSSLNLSVTSFKKIVYREYEPYFKKEKPQSTISGLLGPTLYAEVGDIIXVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1PA6 repeat:
22732. .22827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSq repeat: matches 303. .1 of consensus"
13253. .13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1ME1 repeat:
                                                           protein_id="CAB16748.1"

'db_xref="GI:2769647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MLT1F repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match: H61071 H69565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="THE1C repeat: matches 371. .1 of consensus"
L2196. .12497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="AluY repeat: matches incomplete repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"MER45 repeat: matches 1. .178 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Ll repeat: matches 2577.
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.26378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25381
                                                                                                            actor V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      .2759 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .138 of
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Query Match
Best Local Similarity
Matches 18; Conserv
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       Conservative
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/note="MIR repeat: matches 40. .235 of consensus"
38333. 38451
/note="AluJo repeat: matches 1. .134 of consensus;
1ncomplete repeat"
40215. 40272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDIMRDIASGLIGLLLICKSRSLDRÖGIORAADIEQAVFAVFDENKSWYLEDNINKF
CENPDEWKRDDRKFYESNIMSTINGYVPESITILGFCFDDTVORHFCSVOTQNEILTI
HTTGHSEIVSKRHEDTLIFPHAGESVTVTMDNVOTWALTSMNSSPRSKLRLKERDV
KCIPDDEDSYEIFEPESTVMATRKMHDRLEPEDEESDADYDVONLAAALGIRSFR
KCIPDDEDSYEIFEPPSSTVMATRKMHDRLEPEDEESDADYDVONLAAALGIRSFR
MSLLOBEEEFNLTALALENGTEFVSSNYDIIVSSNYSSPSNIESKTVUNLAEPOKAP
SHOQATTAGSPLRHLIGKNSVLNSSTAEHSSFYSEDPIEDPLQPDVTGIRLLSLGAGE
FKSQEHAKHKGFKVERDOAAKHRESWMKLLAHKVGRHLSQDTGSPSGMREWEDLESQD
TGSPSRNRPWKDPPSDLLLKONNSKKILVGRNHLASERGSFEIDDTDDDTAVNNUT
TGSPSRNRPWKDPPSDLLLKONNSKKILVGRNHLASERGSFEIDDTDDDTAVNNUT
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EDTTYKKVVFRKYLDSTTKRDPRGEYEBHLGILGPI
SLHAHGLSYEKSSEKTYTEDDSPEWFKEDNAVQNSSTTYWHATERSGPESPGSACR
AWAYYSAVNPEKDIHSGLIGPLLICQKGILHKDSNWPMDMREFVLLFMTFDEKKSWYY
EKKSRSSWRLTSSEMKKSHEFHAINGMITSLPGLKWYEDEWYRLHILNIGGSQDIHYV
HFHGQTILENGNKQHDLGVWPLLFSEFKTLEKASKFOWMLLWTEVGEWQRAGMOTPU
LIMDRDCRMPMGLSTGIISDSQIKASEFLGYWEPRLARLNNGGSYNAWSVEKLAAEFA
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KKKKEHTHHAPLSPRTFHPLASEAYNFFSERRLKHSLVLHKSMETSLDTDLNQTLPS
MDFGMIASLDDHNQNISNDTGQASCPPGLYGTPPEEHQQTFPTQDPDQMHSTSDPSH
RSSSPELSEMLEYDRSHKSFPTDISQNSPSSEHEPWQTVISPDLSQTVLSPELSQTNLS
SPDLSHTTLSPELIQRNLSPALGQMPISPDLSHTTLSDLSQTNLSPEL
SQTNLSPALGQWPLSPDLSHTTLSLDESQTNLSPELSQTNLSPELIQRNKDSPALGQMPLSPDLSQTNLSPELIQRNLSPELIGNTLSPELIQRNLSPALGQMPLSPDLSQTNLSPELISPLSQTNLSPE
ISPDLSHTTLSLDFSQTNLSPELSQTNLSPELSHTLSPDSHTTLSLDLSQTNLSPE
ISQTNLSPALGQMPLSPDLSQTNLSPELSQTNLSPE
ISQTNLSPDLSEMPLFADLSQTPLFDDLDQMTLSPDLGETDLSPWFDLSQTNLSPE
ISQTNLSPDLSEMPLFADLSQTPLFDDLDQMTLSPDLGETDLSPWFDDLSQTNLSPE
ISQTNLSPDLSEMPLFADLSQTSPDDLDQTTSPDLGQMPSPS
STILNDTFLSKEPNPLYIVGLSKUGTDVIEITPRESSQSLLLQEFNESFFYPDLGQMPSPS
STILNDTFLSKEPNPLYIVGLSKUGTDVIEITPRESSQSLLLQEFNESFFYPDLGQMPSPS
STILNDTFLSKEPNPLYIVGLSKUGTDVIEITPRESSQSSEDLSQTVPTDDPFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 104. .17 of consensus" 34738. .35036
/note="AluSc repeat: matches 299. .1 of consensus' 35051. .35542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKPWIOVDMOKEVIITGIOTOGĀKHYLKSCYTTEFYVAYSSNOINWOIFKGNSTRNVM
YFNGNOBASTIKENOFDPIVARYIRISTRAYNRPTLKIELGOGEVNGCSTPICHEN
GKIENNOITASSFKKSWMGDYNEPFRAKLNAGORVNAWOAKANNNKOWLEIDLLKIKK
ITAIITOGCKSLSSEMYVKSYTIHYSEOGVEWKPYRLKSSMVDKIFEGNTNTKGHVKN
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DESKSWSQSSSLMYTVNGYVNGTMPDITVCAHDHISWHLLGMSSGPELFSIHFNGQVL
EQNHHKVSAITLVSATSTTANMTVGPEGKWIISSLTPKHLQAGMQAYIDIKNCPKKTR
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KVMYTQYEDESFTKHTVNPNMKEDGILGPIIRAQVRDTLKIVFKNMASRPYSIYPHGV
                                                                                                                                   46627. 46980
/note="LIMA7 repeat: matches 2. .364 of consensus"
46983. 47446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"MIR2 31903. .3198
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                                                                                                                                                                                                              /note="L1 repeat: matches 3613. .5390 of consensus"
46627. .46980
                                                                                                                                                                                                                                                                              /note="LIMA8 repeat: matches 1038. .944 of consensus" 44951. .46774
                                                                                                                                                                                                                                                                                                                                                     /note="MIR2 repeat: matches 146. .93 of consensus"
43456. .43548
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MADE1 repeat: matches 1. .53 of consensus"
43274. .43327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 75. .259 of consensus"
29041. .29084
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incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1 repeat: matches 3215. .3729 of consensus"
                                   8.8%; Score 18; DB
100.0%; Pred. No. 17;
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          Indels
          0; Gaps
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β δ

1250 TAATAAGAAAACATCTAC 1233

171 TAATAAGAAAACATCTAC 188

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Matches 18
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Homo sapiens chromosome 11 clone CMB9-21K9 map 11q22, WORKING SEQUENCE, 25 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 132291 bases at least Q40
Consensus quality: 133603 bases at least Q30
Consensus quality: 133733 bases at least Q20
Estimated insert size: 133783; sum-of-contigs estimation
Estimated insert size: 233000; pulse field gel estimation
Quality coverage: 4.87x in Q20 bases; pulse field gel estimation
Quality coverage: 8.48x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                ch 8.8%; Score 18; DB 72; Length 133783; Similarity 100.0%; Pred. No. 16; 18; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 5, 2000 this sequence version replaced g1:7212886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 13783)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                            43496 a
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2199L14"
25289 c 24707 g 40291 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujlyama, A., Yada, T., Toyoda, A., Taylor, T.D., Hong-Seog, P., Homo sapiens 139,740 genomic DNA of 11q22 Published Only in DataBase (1999) In press 2 (bases 1 to 139740)
                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On Feb 19, 2000 this sequence version replaced gi:6997652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG: HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:CMB9-21K9.
Homo sapiens
Sequence
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APO00817.2 GI:7007459
HTG; HTGS_PHASE1; HTGS
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1 (bases 1 to 139740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://hgp.gsc.RIKEN.go.jp/
Contact: hattori@gsc.RIKEN.go.jp
Contect: project Information
Center project name: HumDraft11
Center clone name: CMB9-21K9
Center clone name: CMB9-21K9
Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of re Assembly program: Phrap; version 0.990329
Consensus quality: 112677 bases at least Q40
Consensus quality: 125720 bases at least Q20
Insert size: 129024; sum-of-contigs
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Primates; Catarrhini; Hominidae; Homo.
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87385 87886; gap of
87987
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47035 56602: contig of
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1867 77672: contig of 5806
7673 78174: gap of 502 bg
8175 81813: contig of 3639
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                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                'clone="CMB9-21K9"
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92260: contig of 4
2762: gap of 50
97056: contig of 4
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97059: contig or 510 bp
566: gap of 510 bp in
102247: contig of 4681 bp in
513 bp
76 4101 bp ir
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137927: contig of
8.8%;
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139740: contig of
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35777: contig of 999 bp in length
277: gap of 500 bp
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7367: gap of 506 bp
.09928: contig of 2561 bp
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33: gap of 500 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of 505 bp 54: contig of 8647 b
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Score 18;
Pred. No.
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502 bp
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and is derived by analysis of the total score distribution.
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AC018744
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U95626 Homo sapien
ACO18744 Oryza sat
M23166 S.cerevisia
I08122 Sequence 1
I09397 Sequence 5
X15135 Yeast NAT 1
Z74088 S.cerevisia
ACO17747 Homo sapi
ACO18747 Homo sapi
ACO19749 Homo sapi
ACO11021 Homo sapi
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31434 - 31443 37900 - 37968 53303 - 53357 59166 - 59206 63708 - 63998 65200 - 65335 78605 - 78713 92135 - 92137 112377 - 112551 112643 - 112778 134284 - 134309 134914 - 135019 FEATURES LOCATION/QUALIFIERS SOURCE /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3"	Cold Spring Harbor Laboratory, 11 NY 11724, USA Regions with single-strand cover	" មកដ្ឋ	1 (bases 1 to 143068) McCombie, W. R., Wilson, R., Chen, E., Gibbs, R. Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Gnoj, L., de la Bastide, M., Kaplan, N., Greco Muzny, D., Chen, CN., Evans, C., FitzGerald, Porcel, B. M., Dragan, Y., Giacalone, J., Pa, Solinsky, K. A., DeSilva, U., Diaz-Perez, S., Z. Watanabe, M., Doggett, N., García, D. and Sagr Human BAC clone 110P12	(ccr6) genes, complete cds, partial cds, complete seque U95626 U95626.1 GI:2104517 HTG. human. Homo sapiens Eukaryota; Metazoa; Chordat Entheria: Drimates: Catarri	ALIGNMENTS 43068 bp DNA PRI	17 7.9 13271 2 AE001168 17 7.9 23332 42 AE0014464 17 7.9 23332 42 AE014464 17 7.9 35589 9 AE001049 17 7.9 35589 9 AE001049 17 7.9 39752 9 D86993 17 7.9 40677 50 HSAC000099	17 7.9 1795 9 HSX14873 17 7.9 1850 1 ECEXPIR 17 7.9 2415 9 AK001422 17 7.9 2489 9 HSDARC 17 7.9 2775 11 AF055992 17 7.9 2775 11 HSU43899 17 7.9 3068 10 575830	25 18 8.4 182482 43 AC016703 AC016703 Homo sapi 26 18 8.4 186243 52 AC012022 AC012022 Homo sapi 27 18 8.4 195832 78 AC013184 AC019184 Homo sapi 28 18 8.4 216215 10 HSG2266022 AC019184 Homo sapi 29 18 8.4 240327 69 AC022422 AC022422 Homo sapi 30 18 8.4 260270 40 AL135840 AC022422 Homo sapi 31 17 7.9 526 13 G61963 AF100634 Homo sapi 32 17 7.9 1155 39 AF100634 AF100634 Homo sapi
	CDS	mRNA .		CDS		gene CDS	mkna	mRNA
receptor 5 (cers) protein, encoded by GenBank Accession Number U54994, gi 1457946" /codon_start=1 /product="cers" /protein_id="AAB57793.1" /protein_id="AAB57793.1" /protein_id="AAB57793.1" /fdb_xref="GI:2104520" //translation="MDYQVSSPIYDINYYTSEDCQKINVKQIAARLLPPLYSLVFIFG FVGNMLVILLILNCKRLKSMTDIYLLMLAISDLFFLLTVPFWAHYAAAOWDPGNTMCQ LLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFAS LPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGIL	/gene=ccrs* /gene=ccrs* /gene=ccrs* /gene=ccrs*	SVITMLYAVFASVPGILITIKCOKEDSVEVCGPYFPRGWNNFHTIMMNILGLVLLIM VICYSGILKTLLRCRNEKKRHAAVRIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSN CESTSQLDQATQVTETLGMTHCCINPILYAFVGEKFRRYLSVFFRKHITKRFCKQCPV FYRETVDGVTSYNTPSTGEQEVSAGL" join(59531. 59573,6147264785) /gene="ccr5" /gene="ccr5" /gene="ccr5" /product="corf5" /product="corf5" /product="corf5" /product="ccr5" /product="ccr5" /product="ccr5"	/note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2), Accession Number: 1168965" /codon_start=1 / Codon_start=1 / Product="ccr2b" /product="ccr2b" /protein_id="AAB57792.1" /protein_id="AAB57792.1" /db_xref="G1:2104519" /translation="MLSTSRSRFIRNTNESGEEVTTFFDXDYGAPCHKFDVKQIGAQL / LPDLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIXLLNLALBDLLFJTTLPDWAHSA NEWNGNAVELFFCTTFFILTTHOWN AND LEADSCOVEN.	/ WILLIAM CONTROL OF THE CONTROL OF	/gene CC12 /note Confirmed by similarity to Human monocyte /note Confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number U80924, gi 1168965" /codon_start=1 /product="ccr2a" /product="ccr2a" /protein_id="AAB57791.1"	4605649505 /gene="ccr2" /note="corfirmed by similarity to Human monocyte /note="corfirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80924), two alternatively spliced mRNAs." join(4610647046,4825548438)	Join (4005647046,4825549505) /gene="ccr2" /note="confirmed by similarity to Human monocyte /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding A-form carboxyl tail, Accession Number U80924." /product="ccr2a"	: 110P12" j97 irmed by similation protein 1 teant protein 1 teant protein 1 44 924 927 927

gene

CDS

mRNA

Spring Harbor,

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Query Match
Best Local :
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                                                                                                                          82 CIGGICCCCACCITIGCAG 100
 AC018744 216514 bp
Oryza sativa chromosome
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Similarity 100.0%;
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QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="confirmed by similarity to lactoferrin protein, encoded by GenBank Accession Number M73700, gi 186818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement(join(124782 ...124816,126528 ...126717, 127884 ...128068,130006 ...130073,132023 ...132164, 133863 ...134018,135022 ...135075,135890 ...135980, 137445 ...137599,138436 ...138610,139077 ...>139253))
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/gene="lactoferrin"
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Translated sequence exhibits 42% sequence identity to CCR5
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/product="ccr6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="lactoferrin"
/protein_id="AAB57795.1"
/db_xref="GI:2104522"
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/product="ccr6"
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/db_xref="GI:2104521"
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)6642. .97676
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                                                                                                                                                                                            Score 19; DB 11;
Pred. No. 5.2;
. 10
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     clone 15022,
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                     l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-JAN-2000) Lita Annenberg Hazen Genome Center, Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poaceae; Oryza.
1 (bases 1 to 216514)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NAT 7, 2000 this sequence version replaced g1:6730690.

NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is is not known and their order in this sequence as
                                                                                                                            62170
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                                                                                                                                                           /db_xref="taxon:4530"
/chromosome="10"
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1 (bases 1 to 2698)

Lee,F.J., Lin,L.w. and Smith,J.A.

Molecular cloning and sequencing of a cDNA encoding alpha-acetyltransferase from Saccharomyces cerevisis alpha-acetyltransferase from Saccharomyces al
                                                                                                                                               18; Conserv
                                                                                                                                                                                                                                                                                                                                          Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence [1] kindly submitted by F.-J.Lee, 10-APR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-acetyltransferase
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FGTTSGLFGSMAIVLLHATRNDTPFDFILKKVVTKSLEKEYSENFFLNEISNNSFDWL
NFYDEKFGKNDINGLLETAKYRDDVPIGSSNLKEMIISSLSPLEPHSQNEILQYYL"
491 c 533 g 748 t
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QFEDDQLDFHSYCMRKGTPRAYLEMLEWGKALYTKPMYVRAMKEASKLYFQMHDDRLK
RKSDSLDENSDEIQNNGQNSSSQKKKAKKEAAAMNKKKETEAKSVAAYPSDQDNDVFG
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PQLERGYPATFSNYKPLYQRRKSKYSPLLEKYVLDYLSGLDFDQDFIPFIWTNYYLSQ
HFLFLKDFPKAQEYLDAALDHTPTLYBFYILKARILKHLGLDFDGDFIPFIWTNYYLSQ
DRFINCKTYKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASWFIVEQAEAYY
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NTKEYKESIKWFTAALNNGSTUNGIYRDLATLGSGIGDFKNALVSRKKWEAFIGYRA
NWTSLAVADVVNGERQDAINTLSGFEKLAEGKISDSEKYEHSECLMYKKDIMYKAKSU
NQDKLQNVLKHLNDIEPCVFDKFGLLERKATIYMKLGQLKDASIVYRTLIKRNPDNFK
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/protein_id="AAA88728.1"
/db_xref="GI:172028"
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/strain="TD71.8"
/db_xref="taxon:4932"
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'db_xref="SGD:S0002198"
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100.0%; Pr
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Smith, J.A. and Lee, F-J.S.
Isolation, purification, characterizat
of N alpha-acetyltransferase
Patent: EP 0334004-A1 1 27-SED-1989;
Location/Qualifiers
ce 1.2699
     baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                               Sequence
109397
                                                                   SUMAII 3347 bp DNA
Yeast NAT 1 gene for N-terminal acetyltransferase.
X15135
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18; Conserv
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l Similarity 100.0%;
18; Conservative
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                                                acetyltransferase; NAT 1
                                                           X15135.1 GI:4027
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5 from Patent
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492 c 532 g
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                              Paulin, L., S
Unpublished
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                                                                 Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3530)
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S.cerevisiae chromosome
Z74088 Z71256
Z74088.1 GI:1431024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mullen, J.R., Kayne, P.S., Moerschell, R.P., Gribskov, M., Colavito-Shepanski, M., Gruns
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Location/Qualifiers
                   (bases 1 to 3530)
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Ailkkdoshydslalkgidlisvegekodaasyyanairriegasaspicchvlgityr
Ailkkdoshydslalungstikoltadiosoigdeknalvsrkkymeaficyra
NTKEYKESIKWFTAALINGSTIKOLTYDAALIOGOIGDEKNALVSRKKYWEAFICYRA
NWTSLAVAODVNGEROOALNTLSOFEKLAEGKISDSEKYEHSECLWYKNDIMYKAASD
NODKLONTLKHLNDIEPCYPDKFGLLERKATIYMKLGOLDASIYYRTLIKRNPDNEK
YYKLLEYSLGIQGDNKLKKALYGKLEOFPYPRCEPPKFIPLTFLODKEELSKKLREYVL
POLERGVPATFSNYKELYQRRKSKYSPLLEKIYLDYLSGIDPTODDIPFTWTNYYLSO
HFILELKDEPGKAQEYIDAALDHTPTLYEFYILKARILKHLMOTAAGILEEGROLDLO
DRFINCKTVKYFLRANNIDKAPEVASLFTKNDDSYNGIKDLHLVEASWFIVEQAEAYY
RLYLDRKKKLDDLASIKKEVESDKSGOLANDIKENQWLYRKYKGLALKRENAIPKYK
GPEDDOLDBYSYCHRKGTPRAYLEMLEWGKALYTKPMYRAKEASKLYFOMHDDRIK
RKSDSIDENSDEIONNGONSSOKKKAKEAEAAMKRKETEAKSVAAYPSDODNDVFG
EKLLETSTPMEDFATEFYNNYSMOYREDERDYILDFEFNYRIGKLALCFASLNKFAKR
RKSDSIDENSDEIONNGONSSOKKKAKEAEAAMKRKETEAKSVAAYPSDODNDVFG
EKLLETSTPMEDFATEFYNNYSMOYREDERDYILDFEFNYRIGKLALCFASLNKFAKR
FGTTSGLFGSMAIVLHATRNDTFFDDILKKYVTKSLEKSYSNKFDASLNNSTDWL
FGTTSGLFGSMAIVLHATRNDTFFDDILKKYVTKSLEKSYSNKFDASLNNSTDWL
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3330...>3347
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/db_xref="GI:578200"
/translation="MTIPHM"
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/db_xref="GI:4028"
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/db_xref="taxon:4932"
                                                      Saren, A.M. and Laamanen, P
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0; Mismatches
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tein,M., Sherman,F.
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Z71781
Z71781.1 GI:
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       Direct Submission
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Submitted (09-UUL-1996) Data collected by MIPS on behalf of the European yeast chromosome IV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                Saren, A.M., Laamanen, P., Lejarcegui, J.B. and Paulin, L. The sequence of a 36.7 kb segment on the left arm of chromosome IV from Saccharomyces cerevisiae reveals 20 non-overlapping open reading frames (ORFs) including SIT4, FAD1, NAM1, RNA11, SIR2, NAT1, PRP9, ACT2 and MPS1 and 11 new ORFs
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l similarity 100.0%;
18; Conservative
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                                                                                                                                                                                                                                                                                                                                              NAT 1 gene; protein
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1 (bases 1 to 36687)
                       Yeast 13 (1), 65-71 (1997)
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/gene="NAT1"
/db_xref="SGD:S0002198"
complement(419. .2983)
/gene="NAT1"
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FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDWL
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PQLERGYPATTSNYKPLYQRRKSKYSPLLEKIYLDYLGGLDPTODPIPTIWTYLSQ
HELFILKDFPKAQEYLDAALDHTPTLYEFYILKARILKHLGLMDTAAGILEEGRQLDLO
DRFINCKTYKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASWFIVEQAEAYY
RIYLDKKKKLDDLASLKKEVESDKSEQIANDIKENGWLYRKYKGLLKRENAIPKFYK
QFEDDOLDFHSYCMRKGTBRAYLEMLEWGKALYKENGYLAKEENSKLYFOMHDDRLK
RKSDSLDENSDEIQNNGGNSSSQKKKAKKEAAAMNKRKETEAKSYAAYPSDQDNDVFG
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/protein_id="CAA98599.1"
/db_xref="GI:1431025"
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/db_xref="taxon:4932"
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in kinase; protein phosphatase; SIR2 gene; SIT4
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gene		CDS	gene CDS		gene	CDS	JOURNAL FEATURES SOURCE
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CDS	CDS			gene CDS	. CDS		CDS
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/db_xref="SGD:S0002198"

/gene="NAT1" /standard_name="D2720" /note="Acc.no. X15135"

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SOURCE
ORGANISM
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ACCESSION
                                                              COMMENT
                                                                                                                                                                                                                                                                                                                      REFERENCE
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Best Local S
Matches 18
                                                                                                                                                                                                                                                           AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-phosphogluconate dehydrogenase decarboxylating; cell wall protein; class v pyridoxal phosphate dependent aminotransferase; elongation factor g; elongation factor Tu family; fbpl; fructose-1,6-bisphosphatase; 6 beta repeat; glycine-rich protein; low-complexity gene-free region; mik1; mitosis inhibitor protein kinase mik1; myb like dna-binding protein; neutral trehalase; ntpl; polyA-binding protein; rasll; replication factor-a protein 1; ribonucleoprotein; RNA recognition; RNA3' Cleavage factor Ib; rpal; ssbl; transcription initiation factor iif beta subunit; WD domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPBC660 43325 l
S.pombe chromosome
AL034563
                                                                                         Submitted (18-DEC-1998) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Biotechnologische und molekularbiologische Forschung, Angelhofweg 39, D-69259 Wilhelmsfeld, Germany
                                                                                                                                                                                                                                                                                                                Schlzosaccharomyces pombe
Eukaryota; Fung1; Ascomycota; Schlzosaccharomycetales;
Schlzosaccharomycetaceae; Schlzosaccharomyces.
1 (bases 1 to 43325)
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Direct Submission
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Details of yeast sequencing at the Sanger Centre the World Wide Web.
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NFYQEKFGKNDINGLLEVYRDDYPIGSSNLKEMIISSLSPLEPHSQNEILQYYL"
COMPLEMENT (14327. . . 14674)
                                                                                                                                                                                                                                                                                     Rajandream, M.A., Barrell, B.G. and Rieger, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="D2723"
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omosome II cosmid c660.
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Pred. No.
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                                    are available
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misc_feature

/gene="SPBC660.01c"

'note="ttaacgtttag, splice branch and acceptor"

misc_feature

misc_feature

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FEATURES
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During 1995 to 1996 about 66% of S. pombe chromosome I was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the
number of introns/exons or we may not have chosen the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (complementary strand).

(complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c660 is overlapped at the 3' end by cosmid 1198 (contained in EMBL entry SP33010 accession number U33010).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splice donor/acceptor sites.

CDS are numbered using the following system eg SPBC25H2.0lc. SP pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS),
/note="ctaatattttaatttaag, splice branch and accept complement(132. .137)
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/note="gtaagt, splice donor sequence"
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/gene="spBC660.01c"
/note="Match to pF00249 myb_DNA-binding, Myb-like
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PKTIRMFYSNLYKKLSHRDAKSIYHYRRAYNFEDLSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SPBC660.01c, SIMILARITY:Schizosaccharomyces pombe,
CAB52717, putative myb-like dna-binding protein., (496
aa), fasta_scores: opt: 478, E():4.7e-23, (30.6% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1. .1482)
/gene="SPBC660.01c"
complement(join(1. .86,138. .464,506. .1482))
                                                                                                                                                                                                                                                                                                   complement(87. .104)
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                                                                                                                                                                                                                                                                                                                                                                      pombe chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INWTLVAOMLGTRTRLQCRYKFQQLTKAASKFELQENVWLLERIYDSLLNNGGKIHWE
NIVKEANGRWTRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Schizosaccharomyces pombe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4896"
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                                                                                                                                                                                                                                                                                                                                                                                                           'note="nominal overlap with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="cosmid c660"
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                                                                                                                                                                                                                                                                                                                                                                                                               cosmids SP33010,
                                                                                                                                                                                                                                                                 and acceptor"
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acceptor"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(3930. .4184,4288. .4431,4491. .5015))
/gene_"SPBC560.03c"
/note_"SPBC560.03c, len:307, SIMILARITY:Saccharomyces
/note_"SPBC560.03c, len:307, SIMILARITY:Saccharomyces
cerev isiae, YGR005C, T2FB_YEAST, transcription initiation
factor iif, beta subunit, (400 aa), fasta scores: opt:
461, E():2 .9e-32, (31.0% identity in 368 aa);
SPBC560.03c, len:307, SIMILARITY:Saccharomyces cerevisiae,
T2FB_YEAST, transcription initiation factor iif, beta
subunit, (400 aa), fasta scores: opt: 461, E():1.4e-22,
(31.0% identity in 368 aa)"
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TSSSMKSTALVGTVAHECNVSPVINDDYRRVMQKRALAASAPKRKVQMIDDRGGSLLA
PGTLGSRSRSTTSFIRNVKPRTGEGLKNSRIPRNELLDILFKCFEDVEYWTLKGLREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDFGATNHVTSVLMTGKGTQLAVGTDSGVIYIMDIESTKSVRSLKGHSERVAALAWND
NTLTSGGKDEVILHHDLRAPGCCAEMKVHEQELGGLQWDRSLGAEGGNDNNLFVW
DYRSSRPLHKEEEHTAAVKAIGWSPHORGILASGGGTIDRCLTHNTLTGRCLQNKDL
GSQVCNMAWSKTSNEIVTTHGFAKNQVSLWKYPSLKNIANLTAHTNRVLYLSMSPDGQ
                                                                                                                                                                                 VKQPEVYLKEVLDSIAILNKRGPYALKYSLKPEYKGTMDAASVELRNQQASQSESSSIDHTGKNTSPDNPGTNAEEDEDDDGVEMIDVV"
complement(4185. .4202)
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2772. .2784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="Sptrembl:094423"
/translation="mgdrfiptringnosptremblshaltion="mgdrfiptringnosptremblshaltion="mgdrfiptringnosptremblishergogabarsafyygebrekeriekkmldtpdrksyslsptibposodmlropokerrafpkrtpykildapylkndfylnlldmgosnvlavglassiylmsaasgkvyol
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/gene-"SPBC660.02"

/note-"SPBC660.02, len:421, SIMILARITY:Schizosaccharomyces
pombe, Ol3386, srwl., (556 aa), fasta scores: opt: 1364,
E():0, (50.6% identity in 385 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Match to PF00400 WD40, Score 20.22"
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/gene="SPBC660.03c"
/note="gtatgt, splice donor sequence"
                                                                                                            /note="ctaatgaattcatattag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transcription initiation factor iif, beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPBC660.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Match to PF00400 WD40,
Score 31.68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Match to PF00400 WD40,
score 22.93"
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/protein_id="CAA22522
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2618. .3929
                                                                                                                                            'gene="SPBC660.03c"
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/label=SPBC660.03c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="ctaacgacagcag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPBC660.02"
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2.1"
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                                                                                                                branch
                                                                                                            and acceptor"
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VERSION
KEYWORDS
SOURCE
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AC022747/c
       COMMENT
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Best Local S
Matches 18
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TITLE
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                                                                           JOURNAL
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les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                         Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Dewar, E., Domino, M., Doyle, M., Fenestor, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marthand, J., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marthand, J., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marthand, J., Marthand, J., Marthand, J., Marthand, McKernan, K., Marthand, McKernan, McKern
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                      McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Stricell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 83536)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-131K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                            Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases
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/note="ctaactttttttcag, s
complement(4485...4490)
/gene="SPBC660.03c"
/note="gtatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6066. .6833)
/gene="SPBC660.04c"
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/baxef="GI:4049503"
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KSNGCCKLIVSEEEEDLIVVDSNGSYAVTCDPIDGSSNIDAGVSVGTIFGIYKLRPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAYPCSKGNNGKLRLLYECFPMAFLVEQAGGIAVNDKGDRILDLVPKTLHGKSSIWLG
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/gene="SPBC660.04c"
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complement(6039. .7082)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SPBC660.04c"
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/db_xref="taxon:9606"
/chromosome="11"
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Submitted (03-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 21, 2000 this sequence version replaced gi:6862782.

------Genome Center

Center: Joint Genome Institute

Center: Joint Genome Institute

Total Company Center Center Code: JGI

Web site: http://www.jgi.doe.gov
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Homo sapiens chromosome
30 unordered pieces.
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18; Conserv
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Consensus quality: 118702 bases at least Q30
Consensus quality: 130365 bases at least Q20
Consensus quality: 133293 bases at least Q20
Estimated insert size: 141107; sum-of-contigs estimation
Estimated insert size: 149000; pulse field gel estimation
Quality coverage: 3.58x in Q20 bases; pulse field gel estimation
Quality coverage: 3.78x in Q20 bases; sum-of-contigs estimation
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1 (bases 1 to 141107)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                be preserved.
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59597: contig of 7251 bp in length

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/note="L1 repeat: matches 5390. .5194 of consensus"
2854. .3352
/note="L1ME1 repeat: matches 60"
2971. .3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"L
6468. .65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3327. .3559 ----- matches 2/v. .1/v of consensus /note="MER20 repeat: matches 1. .218 of consensus" 3580. .3873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusq repeat: matches 303. .1 of consensus" 13253. .13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1876. .2745
/note="L1MB5 repeat: matches 921. .1 of consensus"
2597. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1410. .1587
/note="MLT1D repeat: matches 139.
1575. .1858
/note="match: multiple ESTs; match: R71060 H69028 R82016 R10102 R82280 R82281; match: R82066 H69792 H79486 AA506861 R10102 R82280 R82281; match: R82066 H69792 H79486 AA506861 R78091; match: W03874 H74282 D85329" Complement(join(27431 . 27577,28562 . .28744,31530 . .31681,33638 . .33782,36315 . .36470,36919 . .37022,37955 . .38026,39019 . .39135,41033 . .41212,42726 . .4236,43904 . 44440,49524 . .449786,53412 . .56232,57414 . .73672 . .73884,85339 . .85461,69764 . .69985,72271 . .72414,73672 . .73884,85339 . .85461,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR2 repeat: matches 4...127 of consensus"
13398...15749
...note="L1 repeat: matches 2577...4940 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  25527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="THE1C repeat: matches 371.
12196. .12497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 89. .262 of consensus" complement(10749. .11106) /note="match: STS G05144" 11725. .12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSc repeat: matches 2.
10054. .10223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7024. .7238
/note="AluY repeat:
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"AluSc repeat: matches 1. .299 of consensus" 3877. .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                      <25068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR2 repeat: matches 22. .145 of consensus"
                                                                                                                                                                                                                                                                             /note="MLT1F repeat: matches 18.
26055. .26264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16076. .16554
/note="L1 repeat: matches 4910. .5390 of consensus"
16409. .17294
                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MB5 repeat: matches 812.
<25068. .25543</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1PA6 repeat: matches 1. .890 of consensus"
22732. .22827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PA2 repeat: matches 1. .891 of consensus" 7808. .19825
                                                                                                                                                                                                                                                                                                                                                                                                                              e-"match: H61071 H69565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -"L1MB4 repeat: matches 797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ="L1 repeat: matches 3338. .5390 of consensus"
3. .20571
                                                                                                                                                                                    "LIMA7 repeat: matches 1017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1MC2 repeat:
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                                                                                                                                                                                                                                                       repeat: matches 2971. .2759 of consensus"
                                                                                                                                                                                                                                                                                                                                         repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matches 84. .299 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 265.
                                                                                                                                                                                                                                                                                                                                                                                      .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .295 of consensus"
                                                                                                                                                                                                                                                                                                   .138 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .922 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .902 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .323 of consensus"
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HFTGHSFIYGKRHEDTLTLFPMRGESVTVTMDNVGTWMLTSMNSSPRSKKLÄLKFRDV
KCIPDDEDSYEIFEDPESTVAATRKMIDRLEDEDESSDADYDVGVRLAAALGIRSFR
NSSLNQEEBERLITALALENGTETVSSNTDIIVGSNYSSPSNISKFTVNMLAEPOKAS
SHQQATTAGSPLRHLIGKNSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIRLLSLGAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFSPYEDEVNSSFTSGRNNTMIRAVQPGETYTYKWNILEFDEPTENDAQCLTRPYYSD
VDIMRDIASGLIGLLLICKSRSLDRQGIQRAADIEQQAVFAVFDENKSWYLEDNINKF
CENPDEVKRDDPKFYESNIMSTINGYVPESITTLGFCFDDTVQWHFCSVGTQNEILTI
                                                                                     EKKSRSSWRLTSSEMKKSHEFHAINGMIYSLPGLKMYEQEWVRLHLLNIGGSQDIHVV
HFHGQTLLENGNKQHQLGVWPLLPGSFKTLEMKASKPGWWLLNTEVGENQRAGMQTPF
LIMDRDCRMPMGLSTGIISDSQIKASEFLGYWEPRLARLNNGGSYNAWSVEKLAAEFA
SKPWIQVDMQKEVIITGIQTQGAKHYLKSCYTTEFYVAYSSNQINWQIFKGNSTRNVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLSPDISDITLLPDLSQISPPPDLDQIFYPSESSQSLLLQEFNESFPYPDLGQMPSPS
SPTLNDTFLSKEFNPLVIVGLSKDGTDYIEIIPKEEVQSSEDDYAEIDYVPYDDPYKT
DVRTNINSSRDPDNIAAWYLRSNNGNRRNYYIAAEEISWDYSEFVQRETDIEDSDDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTNLSPALGOMPLSPDLSHTTLSLDFSQTNLSPELSHWTLSPELSQTNLSPALGOMP
ISPDLSHTTLSLDFSQTNLSPELSQTNLSPALGOMPLSPDPSHTTLSLDLSQTNLSPE
LSQTNLSPDLSEMPLFADLSQIPLTPDLDQMTLSPDLGETDLSPNGGQMSLSPDLSQV
GK I ENKQITASSFKKSWWGDYWEPFRARLNAQGRVNAWQAKANNNKQWLEIDLLKIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPDLSHTTLSPELIQRNLSPALGQMPISPDLSHTTLSPDLSHTTLSLDLSQTNLSPEL
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RSSSPELSEMLEYDRSHKSFPTDISQMSPSSEHEVWQTVISPDLSQVTLSPELSQTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKSQEHAKHKGPKVERDQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRPWEDLPSQD
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/protein_id="CAB16748.1"
/db_xref="GI:2769647"
                                                                                                                                                                                                                                                                                                       AWAYYSAVNPEKDIHSGLIGPLLICQKGILHKDSNMPMDMREFVLLFMTFDEKKSWYY
                                                                                                                                                                                                                                                                                                                                                                                                                  edttykkyvfrkyldstftkrdprgeyeehlgilgpiiraevddviqvrfknlasrpy
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ISPQNASRAWGESTPLANKPGKQSGHPKFPRVRHKSLQVRQDGGKSRLKKSQFLIKTR
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TRPEPINSSLNLSVTSfKKIVYREYEPYfKKEKPQSTISGLLGPTLYAEVGDIIKVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="SPTREMBL:043737"
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31903. .31988 /note="MIR repeat: matches 104. .17 of consensus" 34738. .35036 27629 ...27788 /note="AluJo repeat: matches incomplete repeat" 28002. .28176 /note="L1MA8 repeat: matches 1038. .944 of consensus" 44951. .46774 /note="MADE1 repeat: matches 1. 43274. .43327 /note="AluSc repeat: matches 299. .1 of consensus" 35051. .35542 /note="11 repeat: matches 3613. 46627. 46980 /note="11MA7 repeat: matches 2. 46983. .47446 incomplete repeat" 10215. .40272 38333. .38451 /note-"AluJo repeat: matches 1. /note="L1 /note="MIR repeat: matches 75. .259 of consensus" 'note="MIR2 repeat: matches 146. .93 of consensus" 'note-"MIR2 note="MIR repeat: matches 40. .235 of consensus" .29084 1KZ repeat: matches 103. l repeat: matches 3215. .3729 of consensus^{*} 36808 302. .364 of consensus" .53 of consensus .134 of consensus; .5390 of consensus" .146 of consensus" .140 0f consensus;

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TITLE
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TITLE
                                                                                        Matches
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                     62087 AAAACATCTACTTTGAAA 62104
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                                                    187 AAAACATCTACTTTGAAA 204
                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus quality: 132291 bases at least Q40
Consensus quality: 133293 bases at least Q30
Consensus quality: 133633 bases at least Q20
Estimated insert size: 133733 bases field gel estimation
Estimated insert size: 233000; pulse field gel estimation
Quality coverage: 4.87x in Q20 bases; pulse field gel estimation
Quality coverage: 8.48x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 5, 2000 this sequence version replaced g1:7212886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 5 closeQUENCE, 2 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence, It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                        43496
                                                                                        Conservative
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                                                                                                                                                                                 /chromosome="5"
/clone="CTD-2199114"
25289 c 24707 g 40291 t
                                                                                                                                                                                                                                                                                        1 9662: contig of 9662 bp in length gap of unknown length 3 133783: contig of 124121 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; Pr
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100.0%;
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Primates;
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; Pred. No. 19;
                                                                                                    Score 18;
Pred. No.
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5 clone CTD-2199L14, WORKING DRAFT
                                                                                        Mismatches
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                                                                                                  DB 72;
19;
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                                                                                                                    Length 133783;
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                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On Feb 19, 2000 this sequence version replaced gi:6997652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ./ 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 139740)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Frujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 139,740 genomic DNA of 1192

Published Only in DataBase (1999) In press

2 (bases 1 to 139740)

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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 11 clone CMB9-21K9
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center clone name: CMB9-21K9

center summary Statistics

Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
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contains that have not been assembled into contains. The second of N are used to separate the reads a did the order in which they appear is completely a bitrary. Low-pass sequence sampling is useful for itentifying clones that hay be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washirgton.edu/RM/RepeatMasker.html
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/note="MLT1E repeat: matches 1. .84 of consensus"
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HS86F14/c
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JOURNAL
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KEYWORDS
SOURCE
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AL SUDMILECT SUDMILESTON

AL SUDMILECT (08-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

NAPY 9, 2000 this sequence version replaced gi:7320935.

IMPORTANT This sequence to unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in

progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be coitaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Contig_ID: 00643 Length: 7736bp
Contig_ID: 00773 Length: 7757bp
Contig_ID: 00773 Length: 76087bp.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* this record will be updated with the finished sequence

* this record will be updated with the accession number will

* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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6 clone RP1-278E11, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                             DB 51; Length 83536; 20;
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unknown length
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0; Mismatches
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Homo sapiens chromosome 6 clone F
PROGRESS ***, 3 unordered pieces.
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/db_xref="taxon:9606"
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AL136089.9 GI:7530184
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57264:
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DEFINITION
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VERSION
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TITLE
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SOURCE
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COMMENT

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Cambridgeshire, CB10 18.4, WR. E-mail enquires:
Cambridgeshire, CB10 18.4, UK. E-mail enquires:
Cambridgeshire, CB10 18.4, UK. E-mail enquires:
Cambridgeshire, CB10 18.4, UK. E-mail enquires:
humquery@sanger.ac.uk/HGPChrily.
Sanger Centre, Hinton.
In Morrant:
In 1998 this sequence version replaced gi:2578147.
It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections neighbouring submissions.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 http://www.sanger.ac.uk/HGP/Chrl/
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence has not repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature by the real or sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS86F14 106571 bp DNA PRI 23-NOV-1999
Human DNA sequence from PAC 86F14 on chromosome 1q23-1q24. Contains
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The true right end of clone 86F14 is at 106571.

S6F14 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                          Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106571)
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/note="AluSx repeat: matches 1. .302 of consensus"
1270. .1360
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19;
                                                                            1600 others
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Submitted (13-JAN-1998) Chromosome 1 Project Group
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/clone="RPI-278E11"
/clone_lib="RPCI-1"
22682 c 22914 g 27418 t
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/clone="RP1-86F14"
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                                                                                                                                                                                                                                                                                                                                                           197 CTTTGAAACATCTACTGG 214
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                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 18; Conservative
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